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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypep-
tides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.FILE COPY
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DESCRIPTION

PROTEIN KINASES

FIELD OF THE INVENTION

5 The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10 The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

 Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key
15 biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

 Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:
20 cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the
25 etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

 The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism
30 includes changes in the catalytic properties (V_{\max} and K_m) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple
20 alignment of the sequences in the catalytic domain of protein kinases and subsequent parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

We have recently completed a systematic analysis of the protein kinases present in
25 *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

Using parsimony analysis, the protein kinases may be divided into 4 major groups:
30 AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungus-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5 The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

10 The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca²⁺/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

15 CMGC group kinases are "proline-directed" enzymes phosphorylating residues that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

20 The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

25 Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EFKs); homologues of the yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close
30 homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD_sp, YGR262_sc) kinases, and others that are "unique" and don't cluster into any obvious family.

SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

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SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
5 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides
conjugated to each other, including DNA and RNA, that is isolated from a natural source
10 or that is synthesized. The isolated nucleic acid of the present invention is unique in the
sense that it is not found in a pure or separated state in nature. Use of the term "isolated"
indicates that a naturally occurring sequence has been removed from its normal cellular
(i.e., chromosomal) environment. Thus, the sequence may be in a cell-free solution or
placed in a different cellular environment. The term does not imply that the sequence is
15 the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at
least) of non-nucleotide material naturally associated with it, and thus is distinguished
from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the
specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of
20 the total DNA or RNA present in the cells or solution of interest than in normal or
diseased cells or in the cells from which the sequence was taken. This could be caused by
a person by preferential reduction in the amount of other DNA or RNA present, or by a
preferential increase in the amount of the specific DNA or RNA sequence, or by a
combination of the two. However, it should be noted that enriched does not imply that
25 there are no other DNA or RNA sequences present, just that the relative amount of the
sequence of interest has been significantly increased. The term "significant" is used to
indicate that the level of increase is useful to the person making such an increase, and
generally means an increase relative to other nucleic acids of about at least 2 fold, more
preferably at least 5 to 10 fold or even more. The term also does not imply that there is no
30 DNA or RNA from other sources. The other source DNA may, for example, comprise
DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term
distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6 -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

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SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
5 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
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SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
10 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
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SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional
15 derivatives thereof as described herein. For sequences for which the full-length sequence
is not given, the remaining sequences can be determined using methods well-known to
those in the art and are intended to be included in the invention. In certain aspects,
polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide
can be encoded by a full-length nucleic acid sequence or any portion of the full-length
20 nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By
“functional” domain is meant any region of the polypeptide that may play a regulatory or
catalytic role as predicted from amino acid sequence homology to other proteins or by the
presence of amino acid sequences that may give rise to specific structural conformations
(*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but
25 not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from
the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
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NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding
20 full-length amino acid sequence, or fragments thereof. A sequence that is substantially
similar to a sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
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NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95%
15 and most preferably 99-100%) to a sequence selected from the group consisting of those
set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ
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ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 or portions of or the entire corresponding full-length amino acid sequences.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) Nucleic Acids Res. 25:3389-3402), Blast2 (Altschul, *et al.* (1990) J. Mol. Biol. 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) J. Mol. Biol. 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID

NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
 NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
 5 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
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 NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
 NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
 NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
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 NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
 NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
 NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
 15 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
 NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
 NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
 NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
 NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
 20 NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
 NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
 NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
 25 ID NO:242, except that it lacks one or more, but not all, of a domain selected from the
 group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a
 coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-
 terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a
 polypeptide having an amino acid sequence selected from the group consisting of those set
 30 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
 NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
 NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of

those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, 5 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, 10 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, 15 SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, 20 SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, 25 SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, 30 a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
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5 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
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10 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
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SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
15 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
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SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at
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100%) to the sequence selected from the group consisting of those set forth in SEQ ID
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NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
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NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
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NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
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NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
10 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
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sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
20 NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
25 NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
30 NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

5 The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

10 The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

15 The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) J. Biol. Chem. 270, 29071-29074).

20 The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein

25 the N-terminal domain can be identified.

30

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further, 10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate 20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine 25 amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of 30 the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

domain may play a regulatory role is PAK3 which contains a heterotrimeric G_i subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic α -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein-protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).
5 Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of
10 the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein
15 database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these
20 methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the
25 protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of
30 the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4 , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

5 The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding
10 a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field,
15 detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes,
20 the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

25 In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19,
30 SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
5 NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
15 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.
25 In particular, a unique nucleic acid region is preferably of mammalian origin and
preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of
nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is
selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe
contains a nucleotide base sequence that will hybridize to a sequence selected from the
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the
genomic regulatory elements, or may be under the control of exogenous regulatory
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
5 NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID
NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
10 NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the
corresponding full-length amino acid sequence. By "fragment," is meant an amino acid
sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least
10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the
group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
15 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
20 SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
25 SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
30 SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
5 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-
length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase
polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ
10 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ
15 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
20 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
25 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
30 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

5 By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is
10 the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or
15 diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that
20 there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in
30 purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (*e.g.*, in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5 In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, 10 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, 15 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, 20 SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, 25 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, 30 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242 where the domain is selected from the group consisting of an N-terminal domain,
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
5 SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it
lacks one or more, but not all, of the domains selected from the group consisting of a C-
terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich
10 region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain
demarcations of the polypeptides of the invention are indicated in Table 2 by reference to
the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in
the art. The natural source may be mammalian, preferably human, blood, semen, or tissue,
15 and the polypeptide may be synthesized using an automated polypeptide synthesizer. The
isolated, enriched, or purified kinase polypeptide is preferably selected from the group
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
20 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ
25 ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ
30 ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ
ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

10 In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By "recombinant kinase polypeptide" is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By "specific binding affinity" is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term "specific binding affinity" describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term "polyclonal" refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

"Monoclonal antibodies" are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term "antibody fragment" refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

5 An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

10 Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may
15 be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

20 In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
25 NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
30 NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242. The binding agent is preferably a purified antibody that recognizes an epitope
present on a kinase polypeptide of the invention. Other binding agents include molecules
that bind to kinase polypeptides and analogous molecules that bind to a kinase
15 polypeptide. Such binding agents may be identified by using assays that measure kinase
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a
kinase polypeptide of the invention or an equivalent sequence. The method involves
identifying the novel polypeptide in human cells using techniques that are routine and
20 standard in the art, such as those described herein for identifying the kinases of the
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)
measuring the activity of said polypeptide; and (c) determining whether said substance
modulates the activity of said polypeptide.

20 The term “modulates” refers to the ability of a compound to alter the function of a
kinase of the invention. A modulator preferably activates or inhibits the activity of a
kinase of the invention.

 The term “activates” refers to increasing the cellular activity of the kinase. The
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is
25 preferably the interaction with a natural binding partner.

 The term “modulates” also refers to altering the function of kinases of the
invention by increasing or decreasing the probability that a complex forms between the
kinase and a natural binding partner. A modulator preferably increases the probability that
such a complex forms between the kinase and the natural binding partner, more preferably
30 increases or decreases the probability that a complex forms between the kinase and the
natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term "complex" refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules
5 bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term "natural binding partner" refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase
10 and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term "contacting" as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution
15 comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

20 In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131,
25 SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,
30 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
10 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
15 and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change
in cell phenotype or the interaction between said polypeptide and a natural binding
partner.

The term “expressing” as used herein refers to the production of kinases of the
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic
20 acid vector is transfected into cells using well known techniques in the art as described
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal
condition by administering to a patient in need of such treatment a substance that
modulates the activity of a polypeptide selected from the group consisting of SEQ ID
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term "preventing" refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5 The term "treating" refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

10 The term "therapeutic effect" refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating efficacy against abnormal conditions can be identified as described herein.

15 The term "abnormal condition" refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in normal cell cycle progression through mitosis and meiosis.

20 Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

25 Abnormal differentiation conditions include, but are not limited to neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

30 Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the protein kinases could lead to cell immortality or premature cell death.

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

5 ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
10 ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
15 ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe
comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the
complements of the sequences and fragments; and (b) detecting the presence or amount of
20 the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from
the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, organ
transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative
stress-related neurodegenerative disorders, metabolic disorder including diabetes,
25 reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group
consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID
NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ
ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID
30 NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20,
SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID
5 NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID
NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID
10 NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID
NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID
15 NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding
full-length amino acid sequence, or a functional derivative thereof. Hybridization
20 conditions should be such that hybridization occurs only with the kinase genes in the
presence of other nucleic acid molecules. Under stringent hybridization conditions only
highly complementary nucleic acid sequences hybridize. Preferably, such conditions
prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20
contiguous nucleotides. Such conditions are defined *supra*.

25 Hybridization conditions should be such that hybridization occurs only with the
genes in the presence of other nucleic acid molecules. Under stringent hybridization
conditions only highly complementary nucleic acid sequences hybridize. Preferably, such
conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20
contiguous nucleotides. Such conditions are defined *supra*.

30 The diseases for which detection of kinase genes in a sample could be diagnostic
include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in
comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

"Amplification" as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722
10 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris
15 *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432
30 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental
5 Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer
Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992);
10 Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular
Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J.
Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol.
15 Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996,
20 incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number
25 WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being
30 treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

5 Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the
10 screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:
15 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is
20 present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).
25 Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse
30 effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
15 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
20 NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting
5 differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include,
10 but are not limited to, those discussed previously.

The term "comparing" as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine
15 these discrepancies in sequences are well-known to one of ordinary skill in the art. The "control" nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the
20 narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred
25 embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34,
SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ
ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID
NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50,
5 SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ
ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID
NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66,
SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ
ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID
10 NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82,
SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ
ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID
NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98,
SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103,
15 SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108,
SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113,
SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,
SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

20 DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding
such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides,
assays utilizing such polypeptides, and methods relating to all of the foregoing. The
present invention is based upon the isolation and characterization of new kinase
25 polypeptides. The polypeptides and nucleic acids may be produced using well-known and
standard synthesis techniques when given the sequences presented herein.

I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the
30 herein-described isolated nucleic acid molecules. The degeneracy of the genetic code
permits substitution of certain codons by other codons that specify the same amino acid
and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13,
SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ
ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID
NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29,
5 SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ
ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID
NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45,
SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ
ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID
10 NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61,
SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ
ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID
NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77,
SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ
15 ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID
NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93,
SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ
ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID
NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID
20 NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID
NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide
or polynucleotide may be used in this regard, provided that its addition, deletion or
substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123,
25 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
30 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded
by the nucleotide sequence. For example, the present invention is intended to include any
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or
its derivative. Moreover, the nucleic acid molecule of the present invention may, as
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity
25 to promote secretion and/or processing of heterologous proteins encoded by foreign
nucleic acid sequences fused thereto, for example. All variations of the nucleotide
sequence of the kinase genes of the invention and fragments thereof permitted by the
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with
30 codons other than degenerate codons to produce a structurally modified polypeptide, but
one which has substantially the same utility or activity as the polypeptide produced by the
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5 Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.
10 Therefore, these nucleic acid molecules are also part of the invention.

 The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore
15 presumably define new protein kinase groups.

 Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

20 II. Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

 A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,
25 Sambrook, Fritsch, & Maniatis, eds., 1989).

 In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain
30 reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

5 In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or
10 primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well
15 known in the art.

III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described
20 nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino
25 acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The
30 polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

5 A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the
10 regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of
15 transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and
20 polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence
25 encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the
30 promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include γ gt10, γ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ , the *bla* promoter of the β -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the α -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ζ -28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

promoters are reviewed by Glick (Ind. Microbiol. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184, π VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: *The Molecular Biology of the Bacilli*, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, *J. Bacteriol.* 169:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater *et al.*, In: *Sixth International Symposium on Actinomycetales Biology*, Akademiai Kiado, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (*Rev. Infect. Dis.* 8:693-704, 1986), and Izaki (*Jpn. J. Bacteriol.* 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, *Miami Wntr. Symp.* 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, *Cell* 28:203-204, 1982; Bollon *et al.*, *J. Clin. Hematol. Oncol.* 10:39-48, 1980; Maniatis, In: *Cell Biology: A Comprehensive Treatise*, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any
5 organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

10 Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

15 One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that
20 can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
25 SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,
30 SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
 SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
 SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
 5 SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
 SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
 SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
 10 SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
 NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of
 these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-
 15 terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are
 provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI,
 CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant
 number of protein kinases that do not belong to any of the known groups, and therefore
 20 presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1,
 Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein

Kinases

The present invention relates to an antibody having binding affinity to a kinase of
 the invention. The polypeptide may have an amino acid sequence selected from the group
 consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
 ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
 30 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
 ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

5 ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ
ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ
ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ
10 ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ
ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ
ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ
ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ
15 ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ
ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ
ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ
ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ
ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ
20 ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or
at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more
contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the
polypeptide not provided in the sequences above, but that is present in the full-length
sequence of the polypeptide and that is easily obtained using methods standard in the art.
25 Further, the antibody may bind specifically to particular domains of one or more of the
kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or
C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to
a kinase or kinase domain of the invention. Such an antibody may be isolated by
30 comparing its binding affinity to a kinase of the invention with its binding affinity to other
polypeptides. Those that bind selectively to a kinase of the invention would be chosen for
use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

5 The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

10 The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

15 The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

20 In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

25 The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

30

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S.
20 Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); McGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune, neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatin, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

5 Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

 Tumor associated: Mok (SEQ ID NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

 Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

15 Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

 Neuronal restricted: CAMKKB (SEQ ID NO:66)

 Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

20 Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

 Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

VIII. Transgenic Animals.

 A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (e.g., the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (Experientia 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO₂ asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, Cell 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

5 In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous
10 kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

15 Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot
20 function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding
25 recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley
30 Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is
10 precipitated with CaPO_4 and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic
25 acid molecule into a cell. Gene transfer is commonly performed to enable the expression of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

15 EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases
Materials and Methods Identification from cDNA databases and isolation of clones
encoding novel protein kinases

Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

25 Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ m TESK2_m	GCTGCTGGACAGTGACT TGTATTT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAACT GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATT TGAAAAT	CTTCATCATCTCTAATACAT TGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 - Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

10

Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

15

PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flt	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

5

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

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The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the *evc* (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

5 Human 5R79-46-1_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- κ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

15 Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

20 Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceeded by the sequence
25 "RGLLAPGDPPCPPNPAPATPPSSRLPTLFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

30 Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

5 Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

10 Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102
15 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

20 Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

25 Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

30 Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324_h orthologue of W30246_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP_057440) used for the Smith-Waterman query): N-term from Incyte 6010175_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175_2, Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides 1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to
15 encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

5 Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015_m (SEQ ID NO: 42, SEQ ID NO:162)

tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The
10 partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

The full-length ORF for R19772 was isolated by screening a cDNA library using a
15 probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

20 Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5 Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10 Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15 Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20 Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

25 Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478_m (SEQ ID NO:80, SEQ ID NO:199)

Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSNGEHGMNPSLQAMMLMGFGDI
FSMNKAGAVMHSGMQINMQAKQNSS
KTTSKRRRGKKVNMALGFSDFDLSEGDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

5 Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

10 Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

15 Human SGK022 orthologue of AA060026_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

20 Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

25 Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP_h 6921333_9; removed intron (146-893) predicted from blastx analysis.

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Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG_040010.

Human orthologue of AA671275_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

5 The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

10 The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

78	92
79	93
80	94
157	193

Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR
5 fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press
10 (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASStar). "DNA
15 Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR
20 fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press
25 (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca ²⁺ /calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

SGK	Serum and glucocorticoid-regulated kinase
STK	serine threonine kinase
ULK	UNC-51-like kinase

The following abbreviations were used for species

H	Human
M	Murine
R	Rat
FV	Fowlpox virus
MT	<i>M. thermoautotrophicum</i>
CE	<i>Caenorhabditis elegans</i>
DM	<i>Drosophila melanogaster</i>
OS	<i>Oryza sativa</i>
SP	<i>Schizosaccharomyces pombe</i>
TP	<i>Tetrahymena pyriformis</i>
PI	<i>Petunia inflata</i>
NC	<i>Neurospora crassa</i>
MSV	<i>Medicago sativa</i>
MSV	Moloney murine sarcoma virus
SA	<i>Squalus acanthias</i>
CS	<i>Cucumis sativus</i>
GM	<i>Glycine max</i>
LL	<i>Lilium longiflorum</i>
TV	<i>Trichomonas vaginalis</i>
MP	<i>Mycoplasma pneumoniae</i>
DD	<i>Dictyostelium discoideum</i>
SC	<i>Saccharomyces cerevisiae</i>
MT	<i>Methanobacterium thermoautotrophicum</i>

Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program (www.ch.embnet.org/software/COILS_form.html). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind (www.at.embnet.org/embnet/tools/bio/PESTfind/). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

Identification of potential coiled-coil domains and PEST domains in N34132

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

C oiled-c il Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

5 Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

10 EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map (http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

15

20

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above, Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

Results

The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

EXAMPLE 3: Generation of Specific Immunoreagents

5 Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

10 Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLKRSQDLPREPLP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLKRKRHYWRLD	507-521
		RHTTRKSSTLRE	488-500
		FQNNTTNRYEKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDVERDEEAVK	375-388
		SPGQGKDHKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPFDWEKTGNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRSM	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VSDSQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDRVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDEDWGS	637-651
		SVSEDPTQLEEVEKD	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein KinasesGENE EXPRESSION ANALYSIS

Tissue Arrays

5 "cDNA libraries" derived from a variety of sources were immobilized onto nylon membranes and probed with 32P-labeled cDNA fragments derived from the gene(s) of interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at each end. An oligo dT primer containing a specific sequence (CDS:
10 AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when it adds additional C residues. If a primer (SMII:
AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G:
15 AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals to the added Cs and the MMLV recognizes the rest of the primer sequence as template and continues transcription. As a result, the synthesized cDNAs contain specific sequence tags at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same sequence (CDS and SMII) it is referred to as "symmetric." When the 5' end is tagged
20 with a different sequence than the 3' end (CDS and ML2G) is referred to as "asymmetric" A double-stranded "cDNA library" is then generated by PCR amplification using the 3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2: AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified "cDNA libraries" were manually arrayed onto nylon membranes
25 with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech) and hybridized with 32P labeled probes generated by random hexamer priming of cDNA fragments corresponding to the genes of interest. After washing, the blots were exposed to phosphorimaging cassettes and the intensity of the signal was quantified. The amount of
30 the DNA on the arrays was also quantified by treating non-denatured or denatured arrays with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2 minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

5 Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AI086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

5

EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

15

Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

20

EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

25

Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

- (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;
- (e) is the complement of the nucleotide sequence of (d);

- (f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;
- (g) is the complement of the nucleotide sequence of (f);
- (h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID
 NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID
 NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID
 NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
 5 NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID
 NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID
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 NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID
 10 NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID
 NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID
 NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID
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 NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID
 NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID
 NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID
 NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID
 20 NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID
 NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID
 NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
 NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not
 all, of the domains selected from the group consisting of an N-terminal domain, a catalytic
 25 domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure
 region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or
 promoter effective to initiate transcription in a host cell.

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4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of
5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
10 SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.
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7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

5 ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
10 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
15 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
20 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
25 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090, N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, 15 AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

5 ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
10 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
15 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
20 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

5 ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
10 ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
15 ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
20 ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from
the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a
spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set
20 forth in: SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
25 NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID
NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID
30 NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID
NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,
5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242 with a test substance;

- (b) measuring the activity of said polypeptide; and
 - (c) determining whether said substance modulates the activity of said
- 25 polypeptide.

30. A method for identifying a substance that modulates kinase activity in a cell comprising:

- (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID
- 30 NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
5 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID
10 NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID
15 NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
20 NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

- (b) adding a test substance to said cell; and
- (c) monitoring a change in cell phenotype or the interaction between
said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

- (a) contacting said sample with a nucleic acid probe which hybridizes
5 under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide
selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
10 SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
15 SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
20 SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
25 SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
30 SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the
nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements
of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

- 5 (b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

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[illegible]

Table 2

Patent Seq ID	Seq ID	Family	Group	Score	Length	ID match	% identity	% Similar	Match	Description	Kinase Domain start	Kinase Domain end	Profile start	Profile end
H 1	122	AGC	GRK	2.7E-314	688	887	100	100	CAR55637.1	Adrenaptic receptor kinase, beta 2 (G-protein-linked receptor like)	181	463	1	261
M 2	123	AGC	GRK	1.30E-190	378	871	98	88	NP 037028.1	Serine/threonine protein kinase [Homo sapiens]	3	143	121	261
H 3	124	AGC	GRK	5.80E-106	419	262	71	86	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	28	288	1	261
H 4	125	AGC	GRK	1.40E-137	414	414	100	100	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	23	283	1	261
H 5	126	AGC	GRK	0	728	728	100	100	NP 037386.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	261
H 6	127	AGC	NDR	1.20E-09	329	73	46	68	BAA70817.1	KIAA0073 protein [Homo sapiens]	35	310	1	261
M 7	128	AGC	NDR	1.30E-19	88	42	49	71	AAF55594.1	CG7719 gene product [Drosophila melanogaster]	24	44	242	261
H 8	129	AGC	NDR	8.10E-181	484	483	100	100	BAA76808.1	KIAA0865 protein [Homo sapiens]	90	383	1	261
H 9	130	AGC	PKC	8.80E-160	978	615	87	80	NP 020233.1	Protein kinase C, mu [Homo sapiens]	651	907	1	261
H 10	131	AGC	PKC	1.10E-10	105	42	57	57	P05127	Protein kinase C, BETA1 TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256	261
H 11	132	AGC	PKC	0	890	890	100	100	NP 005804.1	Protein kinase C, nu [Homo sapiens]	576	832	1	261
M 12	133	AGC	PKC	8.4E-319	889	889	100	100	NP 037487.1	PKNbeta [Homo sapiens]	559	818	1	261
M 13	134	AGC	PKC	1.20E-106	205	204	100	100	JC7083	Protein kinase N beta [Homo sapiens]	1	134	128	261
M 14	135	AGC	SRK	3.80E-12	384	94	36	55	AAC23495.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	81	333	1	261
H 15	136	AGC	SRK	2.90E-257	468	469	100	100	NP 036558.1	Ribosomal protein S6 kinase, 52KD, polypeptide 1 [Homo sapiens]	225	456	1	261
H 16	137	AGC	SRK	7.00E-178	749	745	100	100	NP 055311.1	Ribosomal protein S6 kinase, 90KD, polypeptide 6 [Homo sapiens]	73 & 426	350 & 883	1	261
H 17	138	AGC	SRK	9.80E-222	548	649	100	100	AA030182.1	Unknown [Homo sapiens]	153	538	1	261
M 18	139	AGC	SGK	9.20E-103	431	430	100	100	AA041091.1	SGK [Homo sapiens]	98	355	1	261
M 19	140	AGC	SGK	2.80E-157	430	426	98	99	NP 035491.1	Serum/glucocorticoid induced kinase [Mus musculus]	98	354	1	261
M 20	141	AGC	SGK	2.00E-76	244	244	100	100	AAF12757.2	Protein kinase [Homo sapiens]	1	169	24	261
H 21	142	AGC	SGK	4.10E-211	448	376	88	88	AAF27051.1	SGK-like protein SGK [Homo sapiens]	162	368	1	261
H 22	143	AGC	SGK	5.80E-218	348	349	100	100	NP 009215.1	Protein tyrosine kinase 9-like (AG-related protein) [Homo sapiens]	10	17	253	261
H 23	144	CAMK	AMPK	1.40E-19	440	68	39	61	CAA04119.1	Phosphoprotein [Homo sapiens]	40	333	1	261
H 24	145	CAMK	AMPK	1.50E-165	689	466	65	77	O15075	DCAMK1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1) [Mus musculus]	39	297	1	261
M 25	146	CAMK	CAMK	1.80E-62	297	199	67	83	AAF26875.1	CPG16 [Mus musculus]	415	673	1	261
M 26	147	CAMK	CAMK	2.80E-48	708	181	44	60	O15075	CPG16 [Mus musculus]	514	771	1	261
M 28	148	CAMK	CAMK	2.80E-31	806	147	65	73	AAF26875.1	CPG16 [Mus musculus]	33	293	1	261
H 29	149	CAMK	DAPK	3.10E-121	372	372	100	100	NP 004217.1	Death-associated protein kinase-related 2	32	293	1	261
M 30	150	CAMK	DAPK	7.90E-93	372	340	91	95	NP 004217.1	Death-associated protein kinase-related 2	32	293	1	261
H 31	151	CAMK	DAPK	1.20E-113	414	414	100	100	NP 004751.1	Death-associated protein kinase-related 1	61	321	1	261
H 32	152	CAMK	EMK	5.80E-185	1311	1053	80	80	BAA76843.1	KIAA0899 protein [Homo sapiens]	8	259	1	261
H 33	153	CAMK	EMK	1.20E-45	436	153	61	70	T22427	Hypothetical protein F49C5.4 - [Caenorhabditis elegans]	74	325	1	261
H 34	154	CAMK	EMK	1.40E-32	436	122	46	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	261
M 35	155	CAMK	EMK	1.30E-184	729	728	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	261
M 36	156	CAMK	EMK	3.90E-128	482	482	100	100	AA03487.1	R31237, 1, partial CDS [Homo sapiens]	56	340	1	261
M 37	157	CAMK	EMK	0	1330	1235	100	100	BAA09484.1	KIAA0135 gene, related to p187-1 oncogene, [Homo sapiens]	999	1258	1	261
M 38	158	CAMK	EMK	6.10E-69	230	183	79	85	BAA09484.1	KIAA0135 gene, related to p187-1 oncogene, [Homo sapiens]	1	158	23	261
H 39	159	CAMK	EMK	3.00E-111	926	636	100	100	BAA34501.1	KIAA0761 protein [Homo sapiens]	20	271	1	261
H 40	160	CAMK	EMK	7.30E-80	628	367	57	89	NP 055055.1	KIAA0537 gene product [Homo sapiens]	63	304	1	261
H 41	161	CAMK	MLCK	1.40E-244	714	714	100	100	NP 055401.1	Homonally upregulated neu tumor-associated kinase [Homo sapiens]	61	320	1	261
H 42	162	CAMK	Trio	6.20E-76	874	211	63	80	AA73168.1	Skeletal muscle myosin light chain kinase [Gallus gallus]	570	825	1	261
M 43	163	CAMK	Trio	7.80E-37	127	67	99	99	BAA92535.1	KIAA1297 protein [Homo sapiens]	3	78	186	261
H 44	164	CAMK	Trio	0	1287	1284	100	100	NP 008995.1	STK with Dbl- and pleckstrin homology domains [Homo sapiens]	985	1239	1	261
H 45	165	CAMK	Unique	5.00E-20	514	114	41	63	P25323	MLCK [Drosophila discolorum]	116	381	1	261
H 46	166	CKI	CKI	3.30E-89	508	181	53	65	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	34	313	1	261
H 47	167	CKI	CKI	9.80E-98	478	188	57	68	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	21	471	1	261
H 48	168	CMGC	CDK	9.60E-39	266	138	82	79	NP 036527.1	PFTAIRE protein kinase [Homo sapiens]	1	218	23	261
H 49	169	CMGC	CDK	7.10E-48	247	146	59	75	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	181	23	261

Table 2 (cont'd)

M 50	170	CMGC	CDK	2.90E-64	288	193	65	78	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	240	24	261
H 51	171	CMGC	CDK	1.10E-264	1460	1490	100	100	AAF38401.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H 52	172	CMGC	CDK	9.20E-101	534	377	82	82	AKAMRE	Homo sapiens	4	385	1	261
M 53	173	CMGC	CDK	1.40E-128	337	225	92	96	AAF34871.1	NKX2-1 [Rattus norvegicus]	1	28	235	261
M 54	174	CMGC	CDK	3.00E-48	211	159	78	84	NP 038251.1	Cell cycle related kinase [Homo sapiens]	1	183	134	261
H 55	175	CMGC	CLK	1.50E-242	499	436	81	93	NP 031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	177	493	1	261
H 56	176	CMGC	RCK	9.10E-89	544	343	57	64	AAD12718.1	Extracellular signal-regulated kinase 7, ERK7 [Rattus norvegicus]	13	305	1	261
H 57	177	CMGC	RCK	2.30E-189	419	419	100	100	NP 055041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
H 58	178	CMGC	RCK	1.50E-180	632	832	100	100	AAF31278.1	Intestinal cell kinase [Homo sapiens]	4	284	1	261
M 59	179	CMGC	RCK	1.80E-79	413	188	80	77	P20608	MLCK [Rattus norvegicus]	109	364	1	261
H 60	180	Other	YGR262 ac	2.50E-45	253	102	46	67	AAF50798.1	CG10873 gene product [Drosophila melanogaster]	101	187	65	147
H 61	181	Other	C28C2 ce	2.30E-158	509	258	100	100	CAB70894.1	Hypothetical protein [Homo sapiens]	2	287	1	261
M 62	182	Other	C28C2 ce	1.80E-152	281	243	94	98	NP 0387084.1	Hypothetical protein [Homo sapiens]	59	86	235	261
H 63	183	Other	C28C2 ce	8.70E-300	1852	1193	99	99	NP 055693.1	KIAA0344 gene product [Homo sapiens]	221	479	1	261
H 64	184	Other	C28C2 ce	1.10E-284	535	535	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	73	327	1	261
M 65	185	Other	C28C2 ce	2.50E-208	378	372	98	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
H 66	186	Other	CAMKK	3.80E-148	588	588	100	100	AA031507.1	Ca2+/calmodulin-dependent protein kinase beta [Homo sapiens]	185	448	1	261
H 67	187	Other	GTR1	9.80E-24	287	87	33	52	IG1743	Hypothetical 33.8K protein - rabbit thymus virus	24	285	1	261
H 68	188	Other	DYRK	0	1171	1137	97	99	AA052560.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H 69	189	Other	DYRK	2.10E-280	553	553	100	100	NP 003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	487	1	261
M 70	190	Other	DYRK	2.30E-85	168	149	80	98	NP 003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	76	103	235	261
H 71	191	Other	E1FK	0	1849	1493	80	98	NP 038747.1	GCH2 elf-2alpha kinase [Mus musculus]	280 & 550	539 & 1001	1	261
H 72	192	Other	E1FK	1.50E-220	630	630	100	100	NP 055228.1	Heme-regulated initiation factor 2-alpha kinase [Homo sapiens]	167	583	1	261
H 73	193	Other	Endop	2.50E-45	253	102	46	87	AAF50798.1	CG10873 gene product [Drosophila melanogaster]	101	187	65	147
M 74	194	Other	Endop	3.70E-45	216	102	45	84	AAF50798.1	CG10873 gene product [Drosophila melanogaster]	116	150	116	147
M 75	195	Other	IRAK	0	596	696	100	100	NP 009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	165	443	1	261
M 76	196	Other	IRAK	1.20E-170	392	293	75	85	NP 009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	1	239	19	261
H 77	197	Other	IRE	1.50E-323	922	746	82	89	NP 038148.1	Ins1, insulin-requiring 1 gene [Mus musculus]	518	777	1	261
H 78	198	Other	KYK2 dd	8.70E-40	225	102	45	82	AAF48758.1	CG1173 gene product [Drosophila melanogaster]	32	318	1	261
M 79	199	Other	KYK2 dd	8.90E-32	280	109	32	50	AAF48758.1	CG1173 gene product [Drosophila melanogaster]	12	266	1	261
M 80	200	Other	LIMK	2.80E-17	41	37	92	95	NP 009101.1	Testis-specific kinase 2 [Homo sapiens]	12	39	101	128
H 81	201	Other	MLK	2.50E-282	800	789	100	100	NP 038480.1	Mixed lineage kinase [Homo sapiens]	16	259	1	261
H 82	202	Other	MLK	8.80E-251	835	835	100	100	AA029832.1	Putative protein-tyrosine kinase [Homo sapiens]	463	723	1	261
H 83	203	Other	RIP	2.20E-158	834	385	100	100	BA032317.1	KIAA0472 protein [Homo sapiens]	357	620	1	261
M 84	204	Other	RIP	5.30E-158	289	288	100	100	AAF03133.1	Receptor interacting protein 3 [Mus musculus]	7	27	181	202
H 85	205	Other	SCY1 sc	0	688	688	100	100	CAB55300.1	Hypothetical protein [Homo sapiens]	57	83	50	78
H 86	206	Other	SCY1 sc	1.70E-209	505	354	98	98	BA025981.1	KIAA1380 protein [Homo sapiens]	32	327	1	261
H 87	207	Other	SCY1 sc	2.20E-157	808	396	45	81	AAF58933.1	CG1973 gene product [Drosophila melanogaster]	85	131	47	116
H 88	208	Other	SLOB7	7.40E-196	649	649	100	100	BA091097.1	Unnamed protein product [Homo sapiens]	230	305	81	143
H 89	209	Other	SRPK	5.80E-252	533	533	100	100	NP 055185.1	Serine/threonine kinase 23 [Homo sapiens]	79	531	1	261
H 90	210	Other	STK22A	3.80E-53	268	122	46	70	NP 033461.1	Serine/threonine kinase 22A (spemogenesis associated) [Mus musculus]	10	265	1	261
M 91	211	Other	STK22	2.70E-52	288	127	48	68	NP 033462.1	Serine/threonine kinase 22B (spemogenesis associated)	10	265	1	261
H 92	212	Other	STK22A	4.80E-16	282	112	45	84	NP 033461.1	Serine/threonine kinase 22B (spemogenesis associated)	25	280	1	261
H 93	213	Other	STK22A	5.10E-123	358	322	90	96	NP 033462.1	Serine/threonine kinase 22B (spemogenesis associated)	12	272	1	261
H 94	214	Other	TSK	2.10E-33	273	122	46	62	NP 033461.1	Serine/threonine kinase 22A (spemogenesis associated)	12	287	1	261
H 95	215	Other	TSK	2.50E-32	216	93	41	58	NP 033462.1	Serine/threonine kinase 22B (spemogenesis associated)	1	213	7	261
H 96	216	Other	UNC	0.000062	353	57	36	56	AA032787.1	Putative protein kinase [Rabbits thymus]	1	329	1	261
M 97	217	Other	UNC	0.002482	412	53	37	52	BA07341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	80	408	1	261
H 98	218	Other	UNC	0.001086	341	50	36	66	BA07341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	8	340	1	261
H 99	219	Other	UNC	1.80E-68	480	247	100	100	T17295	Hypothetical protein DKF2p434C131.1 - human (fragment)	57	313	1	261
H 100	220	Other	UNC	1.80E-208	565	468	98	98	BA091270.1	Unnamed protein product [Homo sapiens]	4	265	1	261
H 101	221	Other	Unique	6.70E-10	39	27	69	90	AA000575.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

Table 2 (cont'd)

M 103	222	Other	Unique	0.000022	349	38	30	50	CAA18118.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana]	80	159	1	88
H 104	223	Other	Unique	0.000128	704	54	30	45	BAA88578.1	KIAA1284 protein [Homo sapiens]	1	246	25	281
M 105	224	Other	Unique	0.007385	540	25	42	61	AAF47918.1	Ta protein product [Drosophila melanogaster]	9	104	168	281
H 106	225	Other	Unique	0.31334	540	52	30	42	P10182	SALVARY PROLINE-RICH PROTEIN POLYMER [Homo sapiens]	1	272	18	73
M 107	226	Other	Unique	0.022948	365	25	34	57	NP_006276.1	leucine-specific kinase 1 [Homo sapiens]	68	96	42	71
H 108	227	Other	VRK	3.10E-263	474	474	100	100	BAA80769.1	Vaccinia related kinase 3 [Homo sapiens]	247	318	63	136
M 109	228	Other	VRK	1.20E-111	234	191	82	90	BAA80769.1	(AB031052) vaccinia related kinase 3 [Homo sapiens]	7	78	63	136
H 110	229	Other	YPL235.ac	7.40E-144	305	304	100	100	AAC28337.1	MPSK [Homo sapiens]	20	290	1	281
H 111	230	Other	YQ09.ac	6.10E-49	581	135	43	63	AAF46188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	281
H 112	231	STE	NEK	3.30E-30	698	122	48	67	P51954	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	251	1	281
H 113	232	STE	NEK	2.70E-119	838	357	88	86	AAD31939.1	(AC007059) unknown [Homo sapiens]	52	308	1	281
H 114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004663.1	mitogen-activated protein kinase kinase kinase 6 [Homo sapiens]	378	629	6	281
H 115	234	STE	STE20-02	7.70E-177	718	718	100	100	BAA94194.1	(AB040912) protein kinase PAK5 [Homo sapiens]	449	700	1	281
H 116	235	TK	RTK-20	4.90E-24	485	77	38	56	AA88485.1	(U40827) protein tyrosine kinase [Mus musculus]	187	453	1	281
M 117	236	TK	RTK-20	5.30E-18	183	53	39	57	NP_032036.1	(U40827) growth factor receptor 3 [Mus musculus]	8	143	123	281
H 118	237	AGC	SGK	6.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	262	1	281
H 120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_036261.1	Cell cycle related kinase [Homo sapiens]	4	267	1	281
H 121	239	Other	LMK	8.50E-233	555	555	100	100	NP_009101.1	Tenascin-related kinase 2 [Homo sapiens]	62	293	5	281

WEST

Base	Tumor-glyc	Normal-glyc	Tumor - 1a	Tumor calc	Normal	Endo	p25	SEQ ID NO	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
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165
Table 3 (cont'd)

[illegible]

[illegible]

167
Table 3 (cont'd)[illegible]

WEST

[illegible]

Thesis	Tumor-ym	Mammary-ym	Tumor - fa	Tumor cells	Norral	Ectopic	SES	SEQ M4 YEARS AS ANEG	AS ANEG	AS AMSED	AS ANEG	AS ANEG	AS ANEG	AS ANEG	AS ANEG	AS ANEG	AS ANEG	AS ANEG
Dufano-7								65303	578	729	0	0	0	0	0	0	0	0
Dufano-8								28420	248	374	0	0	0	0	0	0	0	0
Dufano-9								44302	718	136	0	0	0	0	0	0	0	0
Dufano-10								26977	0	633	0	0	0	0	0	0	0	0
Dufano-11								95743	0	496	0	0	0	0	0	0	0	0
Dufano-12								20110	284	211	0	0	0	0	0	0	0	0
Dufano-13								7894	861	23	0	0	0	0	0	0	0	0
Dufano-1								1739	201	54	0	0	0	0	0	0	0	0
Dufano-2								300	1703	253	0	0	0	0	0	0	0	0
Dufano-3								20842	234	0	0	0	0	0	0	0	0	0
Dufano-4								65448	0	11	0	0	0	0	0	0	0	0
Dufano-5								32006	20	0	0	0	0	0	0	0	0	0
Dufano-6								1846	22	0	0	0	0	0	0	0	0	0
ASAB-3								958	212	0	0	0	0	0	0	0	0	0
ADOL-1-6								0	722	0	0	0	0	0	0	0	0	0
HCT-118-7								771	122	55	0	0	0	0	0	0	0	0
HCT-118-8								310	0	144	0	0	0	0	0	0	0	0
HT29-1								0	0	25	0	0	0	0	0	0	0	0
HT29-2								0	0	0	0	0	0	0	0	0	0	0
HT29-3								0	0	0	0	0	0	0	0	0	0	0
GAGS-3								1307	837	26	0	0	0	0	0	0	0	0
SF208-3								3338	7	130	0	0	0	0	0	0	0	0
SF208-4								17078	827	0	0	0	0	0	0	0	0	0
SF-208-7								15222	21	118	0	0	0	0	0	0	0	0
CVCAR-1-7								1233	28	0	0	0	0	0	0	0	0	0
CVCAR-4-8								12786	7	178	0	0	0	0	0	0	0	0
CVCAR-5-7								4723	9	0	0	0	0	0	0	0	0	0
CVCAR-6-8								3134	4	41	0	0	0	0	0	0	0	0
CVCAR-7-9								3472	440	0	0	0	0	0	0	0	0	0
NOCT-7-8								628	0	0	0	0	0	0	0	0	0	0
ADRLS-6								1567	88	0	0	0	0	0	0	0	0	0
PHL-6								1023	717	22	0	0	0	0	0	0	0	0
SW480-7								417	4	71	0	0	0	0	0	0	0	0
SW480-8								0	0	50	0	0	0	0	0	0	0	0
M1289-8								0	22									

170
Table 3 (cont'd)

WEST

171
Table 3 (cont'd)

[illegible]

Table 3 (cont'd)

[illegible]

Table 3 (contd)

[illegible]

174
Table 3 (cont'd)

Tissue	Tumor-type	Metastatic-type	Tumor - %	Tumor count	Normal	Falouts	p53	SEC 84	SEC 104	SEC 126	SEC 143	SEC 157	SEC 171	SEC 185	SEC 199	SEC 213	SEC 227	SEC 241	SEC 255	SEC 269	SEC 283	SEC 297	SEC 311	SEC 325	SEC 339	SEC 353	SEC 367	SEC 381	SEC 395	SEC 409	SEC 423	SEC 437	SEC 451	SEC 465	SEC 479	SEC 493	SEC 507	SEC 521	SEC 535	SEC 549	SEC 563	SEC 577	SEC 591	SEC 605	SEC 619	SEC 633	SEC 647	SEC 661	SEC 675	SEC 689	SEC 703	SEC 717	SEC 731	SEC 745	SEC 759	SEC 773	SEC 787	SEC 801	SEC 815	SEC 829	SEC 843	SEC 857	SEC 871	SEC 885	SEC 899	SEC 913	SEC 927	SEC 941	SEC 955	SEC 969	SEC 983	SEC 997	SEC 1011	SEC 1025	SEC 1039	SEC 1053	SEC 1067	SEC 1081	SEC 1095	SEC 1109	SEC 1123	SEC 1137	SEC 1151	SEC 1165	SEC 1179	SEC 1193	SEC 1207	SEC 1221	SEC 1235	SEC 1249	SEC 1263	SEC 1277	SEC 1291	SEC 1305	SEC 1319	SEC 1333	SEC 1347	SEC 1361	SEC 1375	SEC 1389	SEC 1403	SEC 1417	SEC 1431	SEC 1445	SEC 1459	SEC 1473	SEC 1487	SEC 1501	SEC 1515	SEC 1529	SEC 1543	SEC 1557	SEC 1571	SEC 1585	SEC 1599	SEC 1613	SEC 1627	SEC 1641	SEC 1655	SEC 1669	SEC 1683	SEC 1697	SEC 1711	SEC 1725	SEC 1739	SEC 1753	SEC 1767	SEC 1781	SEC 1795	SEC 1809	SEC 1823	SEC 1837	SEC 1851	SEC 1865	SEC 1879	SEC 1893	SEC 1907	SEC 1921	SEC 1935	SEC 1949	SEC 1963	SEC 1977	SEC 1991	SEC 2005	SEC 2019	SEC 2033	SEC 2047	SEC 2061	SEC 2075	SEC 2089	SEC 2103	SEC 2117	SEC 2131	SEC 2145	SEC 2159	SEC 2173	SEC 2187	SEC 2201	SEC 2215	SEC 2229	SEC 2243	SEC 2257	SEC 2271	SEC 2285	SEC 2299	SEC 2313	SEC 2327	SEC 2341	SEC 2355	SEC 2369	SEC 2383	SEC 2397	SEC 2411	SEC 2425	SEC 2439	SEC 2453	SEC 2467	SEC 2481	SEC 2495	SEC 2509	SEC 2523	SEC 2537	SEC 2551	SEC 2565	SEC 2579	SEC 2593	SEC 2607	SEC 2621	SEC 2635	SEC 2649	SEC 2663	SEC 2677	SEC 2691	SEC 2705	SEC 2719	SEC 2733	SEC 2747	SEC 2761	SEC 2775	SEC 2789	SEC 2803	SEC 2817	SEC 2831	SEC 2845	SEC 2859	SEC 2873	SEC 2887	SEC 2901	SEC 2915	SEC 2929	SEC 2943	SEC 2957	SEC 2971	SEC 2985	SEC 2999	SEC 3013	SEC 3027	SEC 3041	SEC 3055	SEC 3069	SEC 3083	SEC 3097	SEC 3111	SEC 3125	SEC 3139	SEC 3153	SEC 3167	SEC 3181	SEC 3195	SEC 3209	SEC 3223	SEC 3237	SEC 3251	SEC 3265	SEC 3279	SEC 3293	SEC 3307	SEC 3321	SEC 3335	SEC 3349	SEC 3363	SEC 3377	SEC 3391	SEC 3405	SEC 3419	SEC 3433	SEC 3447	SEC 3461	SEC 3475	SEC 3489	SEC 3503	SEC 3517	SEC 3531	SEC 3545	SEC 3559	SEC 3573	SEC 3587	SEC 3601	SEC 3615	SEC 3629	SEC 3643	SEC 3657	SEC 3671	SEC 3685	SEC 3699	SEC 3713	SEC 3727	SEC 3741	SEC 3755	SEC 3769	SEC 3783	SEC 3797	SEC 3811	SEC 3825	SEC 3839	SEC 3853	SEC 3867	SEC 3881	SEC 3895	SEC 3909	SEC 3923	SEC 3937	SEC 3951	SEC 3965	SEC 3979	SEC 3993	SEC 4007	SEC 4021	SEC 4035	SEC 4049	SEC 4063	SEC 4077	SEC 4091	SEC 4105	SEC 4119	SEC 4133	SEC 4147	SEC 4161	SEC 4175	SEC 4189	SEC 4203	SEC 4217	SEC 4231	SEC 4245	SEC 4259	SEC 4273	SEC 4287	SEC 4301	SEC 4315	SEC 4329	SEC 4343	SEC 4357	SEC 4371	SEC 4385	SEC 4399	SEC 4413	SEC 4427	SEC 4441	SEC 4455	SEC 4469	SEC 4483	SEC 4497	SEC 4511	SEC 4525	SEC 4539	SEC 4553	SEC 4567	SEC 4581	SEC 4595	SEC 4609	SEC 4623	SEC 4637	SEC 4651	SEC 4665	SEC 4679	SEC 4693	SEC 4707	SEC 4721	SEC 4735	SEC 4749	SEC 4763	SEC 4777	SEC 4791	SEC 4805	SEC 4819	SEC 4833	SEC 4847	SEC 4861	SEC 4875	SEC 4889	SEC 4903	SEC 4917	SEC 4931	SEC 4945	SEC 4959	SEC 4973	SEC 4987	SEC 5001	SEC 5015	SEC 5029	SEC 5043	SEC 5057	SEC 5071	SEC 5085	SEC 5099	SEC 5113	SEC 5127	SEC 5141	SEC 5155	SEC 5169	SEC 5183	SEC 5197	SEC 5211	SEC 5225	SEC 5239	SEC 5253	SEC 5267	SEC 5281	SEC 5295
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Table 3 (cont'd)

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177
Table 3 (cont'd)

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179
Table 3 (cont'd)[illegible]

180
Table 3 (cont'd)

181

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Tissue	Tissue-cym	Harvest-cym	Tissue - 1g	Tissue-calc	Harvest	Endoth	g/dl	SEG 01 ANGIO 1	SEG 02 ANGIO 2	SEG 03 ANGIO 3	SEG 04 ANGIO 4	SEG 05 ANGIO 5	SEG 06 ANGIO 6	SEG 07 ANGIO 7	SEG 08 ANGIO 8	SEG 09 ANGIO 9	SEG 10 ANGIO 10	SEG 11 ANGIO 11	SEG 12 ANGIO 12	SEG 13 ANGIO 13	SEG 14 ANGIO 14	SEG 15 ANGIO 15	SEG 16 ANGIO 16	SEG 17 ANGIO 17	SEG 18 ANGIO 18	SEG 19 ANGIO 19	SEG 20 ANGIO 20	SEG 21 ANGIO 21	SEG 22 ANGIO 22	SEG 23 ANGIO 23	SEG 24 ANGIO 24	SEG 25 ANGIO 25	SEG 26 ANGIO 26	SEG 27 ANGIO 27	SEG 28 ANGIO 28	SEG 29 ANGIO 29	SEG 30 ANGIO 30	SEG 31 ANGIO 31	SEG 32 ANGIO 32	SEG 33 ANGIO 33	SEG 34 ANGIO 34	SEG 35 ANGIO 35	SEG 36 ANGIO 36	SEG 37 ANGIO 37	SEG 38 ANGIO 38	SEG 39 ANGIO 39	SEG 40 ANGIO 40	SEG 41 ANGIO 41	SEG 42 ANGIO 42	SEG 43 ANGIO 43	SEG 44 ANGIO 44	SEG 45 ANGIO 45	SEG 46 ANGIO 46	SEG 47 ANGIO 47	SEG 48 ANGIO 48	SEG 49 ANGIO 49	SEG 50 ANGIO 50	SEG 51 ANGIO 51	SEG 52 ANGIO 52	SEG 53 ANGIO 53	SEG 54 ANGIO 54	SEG 55 ANGIO 55	SEG 56 ANGIO 56	SEG 57 ANGIO 57	SEG 58 ANGIO 58	SEG 59 ANGIO 59	SEG 60 ANGIO 60	SEG 61 ANGIO 61	SEG 62 ANGIO 62	SEG 63 ANGIO 63	SEG 64 ANGIO 64	SEG 65 ANGIO 65	SEG 66 ANGIO 66	SEG 67 ANGIO 67	SEG 68 ANGIO 68	SEG 69 ANGIO 69	SEG 70 ANGIO 70	SEG 71 ANGIO 71	SEG 72 ANGIO 72	SEG 73 ANGIO 73	SEG 74 ANGIO 74	SEG 75 ANGIO 75	SEG 76 ANGIO 76	SEG 77 ANGIO 77	SEG 78 ANGIO 78	SEG 79 ANGIO 79	SEG 80 ANGIO 80	SEG 81 ANGIO 81	SEG 82 ANGIO 82	SEG 83 ANGIO 83	SEG 84 ANGIO 84	SEG 85 ANGIO 85	SEG 86 ANGIO 86	SEG 87 ANGIO 87	SEG 88 ANGIO 88	SEG 89 ANGIO 89	SEG 90 ANGIO 90	SEG 91 ANGIO 91	SEG 92 ANGIO 92	SEG 93 ANGIO 93	SEG 94 ANGIO 94	SEG 95 ANGIO 95	SEG 96 ANGIO 96	SEG 97 ANGIO 97	SEG 98 ANGIO 98	SEG 99 ANGIO 99	SEG 100 ANGIO 100	SEG 101 ANGIO 101	SEG 102 ANGIO 102	SEG 103 ANGIO 103	SEG 104 ANGIO 104	SEG 105 ANGIO 105	SEG 106 ANGIO 106	SEG 107 ANGIO 107	SEG 108 ANGIO 108	SEG 109 ANGIO 109	SEG 110 ANGIO 110	SEG 111 ANGIO 111	SEG 112 ANGIO 112	SEG 113 ANGIO 113	SEG 114 ANGIO 114	SEG 115 ANGIO 115	SEG 116 ANGIO 116	SEG 117 ANGIO 117	SEG 118 ANGIO 118	SEG 119 ANGIO 119	SEG 120 ANGIO 120	SEG 121 ANGIO 121	SEG 122 ANGIO 122	SEG 123 ANGIO 123	SEG 124 ANGIO 124	SEG 125 ANGIO 125	SEG 126 ANGIO 126	SEG 127 ANGIO 127	SEG 128 ANGIO 128	SEG 129 ANGIO 129	SEG 130 ANGIO 130	SEG 131 ANGIO 131	SEG 132 ANGIO 132	SEG 133 ANGIO 133	SEG 134 ANGIO 134	SEG 135 ANGIO 135	SEG 136 ANGIO 136	SEG 137 ANGIO 137	SEG 138 ANGIO 138	SEG 139 ANGIO 139	SEG 140 ANGIO 140	SEG 141 ANGIO 141	SEG 142 ANGIO 142	SEG 143 ANGIO 143	SEG 144 ANGIO 144	SEG 145 ANGIO 145	SEG 146 ANGIO 146	SEG 147 ANGIO 147	SEG 148 ANGIO 148	SEG 149 ANGIO 149	SEG 150 ANGIO 150	SEG 151 ANGIO 151	SEG 152 ANGIO 152	SEG 153 ANGIO 153	SEG 154 ANGIO 154	SEG 155 ANGIO 155	SEG 156 ANGIO 156	SEG 157 ANGIO 157	SEG 158 ANGIO 158	SEG 159 ANGIO 159	SEG 160 ANGIO 160	SEG 161 ANGIO 161	SEG 162 ANGIO 162	SEG 163 ANGIO 163	SEG 164 ANGIO 164	SEG 165 ANGIO 165	SEG 166 ANGIO 166	SEG 167 ANGIO 167	SEG 168 ANGIO 168	SEG 169 ANGIO 169	SEG 170 ANGIO 170	SEG 171 ANGIO 171	SEG 172 ANGIO 172	SEG 173 ANGIO 173	SEG 174 ANGIO 174	SEG 175 ANGIO 175	SEG 176 ANGIO 176	SEG 177 ANGIO 177	SEG 178 ANGIO 178	SEG 179 ANGIO 179	SEG 180 ANGIO 180	SEG 181 ANGIO 181	SEG 182 ANGIO 182	SEG 183 ANGIO 183	SEG 184 ANGIO 184	SEG 185 ANGIO 185	SEG 186 ANGIO 186	SEG 187 ANGIO 187	SEG 188 ANGIO 188	SEG 189 ANGIO 189	SEG 190 ANGIO 190	SEG 191 ANGIO 191	SEG 192 ANGIO 192	SEG 193 ANGIO 193	SEG 194 ANGIO 194	SEG 195 ANGIO 195	SEG 196 ANGIO 196	SEG 197 ANGIO 197	SEG 198 ANGIO 198	SEG 199 ANGIO 199	SEG 200 ANGIO 200	SEG 201 ANGIO 201	SEG 202 ANGIO 202	SEG 203 ANGIO 203	SEG 204 ANGIO 204	SEG 205 ANGIO 205	SEG 206 ANGIO 206	SEG 207 ANGIO 207	SEG 208 ANGIO 208	SEG 209 ANGIO 209	SEG 210 ANGIO 210	SEG 211 ANGIO 211	SEG 212 ANGIO 212	SEG 213 ANGIO 213	SEG 214 ANGIO 214	SEG 215 ANGIO 215	SEG 216 ANGIO 216	SEG 217 ANGIO 217	SEG 218 ANGIO 218	SEG 219 ANGIO 219	SEG 220 ANGIO 220	SEG 221 ANGIO 221	SEG 222 ANGIO 222	SEG 223 ANGIO 223	SEG 224 ANGIO 224	SEG 225 ANGIO 225	SEG 226 ANGIO 226	SEG 227 ANGIO 227	SEG 228 ANGIO 228	SEG 229 ANGIO 229	SEG 230 ANGIO 230	SEG 231 ANGIO 231	SEG 232 ANGIO 232	SEG 233 ANGIO 233	SEG 234 ANGIO 234	SEG 235 ANGIO 235	SEG 236 ANGIO 236	SEG 237 ANGIO 237	SEG 238 ANGIO 238	SEG 239 ANGIO 239	SEG 240 ANGIO 240	SEG 241 ANGIO 241	SEG 242 ANGIO 242	SEG 243 ANGIO 243	SEG 244 ANGIO 244	SEG 245 ANGIO 245	SEG 246 ANGIO 246	SEG 247 ANGIO 247	SEG 248 ANGIO 248	SEG 249 ANGIO 249	SEG 250 ANGIO 250	SEG 251 ANGIO 251	SEG 252 ANGIO 252	SEG 253 ANGIO 253	SEG 254 ANGIO 254	SEG 255 ANGIO 255	SEG 256 ANGIO 256	SEG 257 ANGIO 257	SEG 258 ANGIO 258	SEG 259 ANGIO 259	SEG 260 ANGIO 260	SEG 261 ANGIO 261	SEG 262 ANGIO 262	SEG 263 ANGIO 263	SEG 264 ANGIO 264	SEG
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Table 3 (cont'd)

Tissue	Tumor-gym	Normal-gym	Tumor-10	Tumor-cells	Normal	Endoth	p53	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
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Table 187
Table 3 (cont'd)

Tissue	Tumor-ym	Normal-ym	Tumor - ls	Tumor cells	Normal	Enrich	pc50	SEQ ID NO
adrenal gland - h		1						84
adrenal node - h		2						85
adrenal node - h		3						86
adrenal node - h		4						87
adrenal node - h		5						88
adrenal node - h		6						89
adrenal node - h		7						90
adrenal node - h		8						91
adrenal node - h		9						92
adrenal node - h		10						93
adrenal node - h		11						94
adrenal node - h		12						95
adrenal node - h		13						96
adrenal node - h		14						97
adrenal node - h		15						98
adrenal node - h		16						99
adrenal node - h		17						100
adrenal node - h		18						101
adrenal node - h		19						102
adrenal node - h		20						103
adrenal node - h		21						104
adrenal node - h		22						105
adrenal node - h		23						106
adrenal node - h		24						107
adrenal node - h		25						108
adrenal node - h		26						109
adrenal node - h		27						110
adrenal node - h		28						111
adrenal node - h		29						112
adrenal node - h		30						113
adrenal node - h		31						114
adrenal node - h		32						115
adrenal node - h		33						116
adrenal node - h		34						117
adrenal node - h		35						118
adrenal node - h		36						119
adrenal node - h		37						120
adrenal node - h		38						121
adrenal node - h		39						122
adrenal node - h		40						123
adrenal node - h		41						124
adrenal node - h		42						125
adrenal node - h		43						126
adrenal node - h		44						127
adrenal node - h		45						128
adrenal node - h		46						129
adrenal node - h		47						130
adrenal node - h		48						131
adrenal node - h		49						132
adrenal node - h		50						133
adrenal node - h		51						134
adrenal node - h		52						135
adrenal node - h		53						136
adrenal node - h		54						137
adrenal node - h		55						138
adrenal node - h		56						139
adrenal node - h		57						140
adrenal node - h		58						141
adrenal node - h		59						142
adrenal node - h		60						143
adrenal node - h		61						144
adrenal node - h		62						145
adrenal node - h		63						146
adrenal node - h		64						147
adrenal node - h		65						148
adrenal node - h		66						149
adrenal node - h		67						150
adrenal node - h		68						151
adrenal node - h		69						152
adrenal node - h		70						153
adrenal node - h		71						154
adrenal node - h		72						155
adrenal node - h		73						156
adrenal node - h		74						157
adrenal node - h		75						158
adrenal node - h		76						159
adrenal node - h		77						160
adrenal node - h		78						161
adrenal node - h		79						162
adrenal node - h		80						163
adrenal node - h		81						164
adrenal node - h		82						165
adrenal node - h		83						166
adrenal node - h		84						167
adrenal node - h		85						168
adrenal node - h		86						169
adrenal node - h		87						170
adrenal node - h		88						171
adrenal node - h		89						172
adrenal node - h		90						173
adrenal node - h		91						174
adrenal node - h		92						175
adrenal node - h		93						176
adrenal node - h		94						177
adrenal node - h		95						178
adrenal node - h		96						179
adrenal node - h		97						180
adrenal node - h		98						181
adrenal node - h		99						182
adrenal node - h		100						183
adrenal node - h		101						184
adrenal node - h		102						185
adrenal node - h		103						186
adrenal node - h		104						187
adrenal node - h		105						188
adrenal node - h		106						189
adrenal node - h		107						190
adrenal node - h		108						191
adrenal node - h		109						192
adrenal node - h		110						193
adrenal node - h		111						194
adrenal node - h		112						195
adrenal node - h		113						196
adrenal node - h		114						197
adrenal node - h		115						198
adrenal node - h		116						199
adrenal node - h		117						200
adrenal node - h		118						201
adrenal node - h		119						202
adrenal node - h		120						203
adrenal node - h		121						204
adrenal node - h		122						205
adrenal node - h		123						206
adrenal node - h		124						207
adrenal node - h		125						208
adrenal node - h		126						209
adrenal node - h		127						210
adrenal node - h		128						211
adrenal node - h		129						212
adrenal node - h		130						213
adrenal node - h		131						214
adrenal node - h		132						215
adrenal node - h		133						216
adrenal node - h		134						217
adrenal node - h		135						218
adrenal node - h		136						219
adrenal node - h		137						220
adrenal node - h		138						221
adrenal node - h		139						222
adrenal node - h		140						223
adrenal node - h		141						224
adrenal node - h		142						225
adrenal node - h		143						226
adrenal node - h		144						227
adrenal node - h		145						228
adrenal node - h		146						229
adrenal node - h		147						230
adrenal node - h		148						231
adrenal node - h		149						232
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adrenal node - h		151						234
adrenal node - h		152						235
adrenal node - h		153						236
adrenal node - h		154						237
adrenal node - h		155						238
adrenal node - h		156						239
adrenal node - h		157						240
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adrenal node - h		161						244
adrenal node - h		162						245
adrenal node - h		163						246
adrenal node - h		164						247
adrenal node - h		165						248
adrenal node - h		166						249
adrenal node - h		167						250
adrenal node - h		168						251
adrenal node - h		169						252
adrenal node - h		170						253
adrenal node - h		171						254
adrenal node - h		172						255
adrenal node - h		173						256
adrenal node - h		174						257
adrenal node - h		175						258
adrenal node - h		176						259
adrenal node - h		177						260
adrenal node - h		178						261
adrenal node - h		179						262
adrenal node - h		180						263
adrenal node - h		181						264
adrenal node - h		182						265
adrenal node - h		183						266
adrenal node - h		184						267
adrenal node - h		185						268
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adrenal node - h		187						270
adrenal node - h		188						271
adrenal node - h		189						272
adrenal node - h		190						273
adrenal node - h		191						274
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adrenal node - h		194						277
adrenal node - h		195						278
adrenal node - h		196						279
adrenal node - h		197						280
adrenal node - h		198						281
adrenal node - h		199						282
adrenal node - h		200						283
adrenal node - h		201						284
adrenal node - h		202						285
adrenal node - h		203						286
adrenal node - h		204						287
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adrenal node - h		207						290
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adrenal node - h		211						294
adrenal node - h		212						295
adrenal node - h		213						296
adrenal node - h		214						297
adrenal node - h		215						298
adrenal node - h		216						299
adrenal node - h		217						300
adrenal node - h		218						301
adrenal node - h		219						302
adrenal node - h		220						303
adrenal node - h		221						304
adrenal node - h		222						305
adrenal node - h		223						306
adrenal node - h								

[illegible]

Table 3 (cont'd)

Tissue	Tumor type	Normal type	Tumor size	Tumor cells	Normal	Endoth	p51	SEQ ID NO
HA-221			155					6
MCF-7ADR-RES			153					6
MCF-7			151					6
IM-14			148					7
UACC-251			147					23
UACC-51			146					9
SK-MEL-28			144					33
UO-31			143					8
SK-MEL-3			142					31
UO-17			141					4
SK-MEL-2			140					283
HCT-116			139					229
MDAMB-231			138					181
COL-205			137					289
LOX-RV1			136					15
SW-620			135					6
TK-10			134					6
HCT-118			133					6
786-T			132					82
MCC-3008			131					79
ACHN			130					278
PC-3			129					6
ROV-385			128					233
HA-M5			127					80
CRL-1			126					276
SR			124					9
AGW			124					137
BP41-R228			123					6
SN12C			122					135
HL-60			121					3
MDA-MB-2			120					116
OVCA-5			119					6
OC-203			118					25
OVCA-8			117					642
CCRF-CEM			116					888
OVCA-3			115					101
SP-439			114					81
MDA-MB-43			113					6
SP-204			112					181
ASHWAYDC			111					111
SP-308			110					113
NCI-H522			109					6
M21			108					204
NCI-H460			107					6
SMB-15			106					20
NCI-H460M			105					430
BAB-19			104					79
NCI-H208			103					66
SK-OV-3			102					8
NCI-H22			101					277
ROV-1			100					6
ROV-1			99					84
OVCA-9			98					6
HOP-82			97					43
U-87MG			96					148
U-87MG			95					219
U-87MG			94					135
ICOP			93					6
AS40-1							yes	5
AS40-2							yes	279
AS40-3							yes	280
AS40-4							yes	247
AS40-5							yes	75
AS40-6							yes	84
EXV-1							yes	280
EXV-2							yes	6
EXV-3							yes	483
EXV-4							yes	877
EXV-5							yes	6
EXV-6							yes	895
EXV-7							yes	213
EXV-8							yes	6
EXV-9							yes	6
EXV-10							yes	344
ADR-RES-1							yes	184
ADR-RES-2							yes	79
ADR-RES-3							yes	115
ADR-RES-4							yes	85
ADR-RES-5							yes	2
ADR-RES-6							yes	263
ADR-RES-7							yes	600
WI-26-1							yes	600
WI-26-2							yes	600
WI-26-3							yes	600
WI-26-4							yes	600
WI-26-5							yes	600
WI-26-6							yes	600
WI-26-7							yes	600
WI-26-8							yes	600
WI-26-9							yes	600
WI-26-10							yes	600
WI-26-11							yes	600
WI-26-12							yes	600
WI-26-13							yes	600
WI-26-14							yes	600
WI-26-15							yes	600
WI-26-16							yes	600
WI-26-17							yes	600
WI-26-18							yes	600
WI-26-19							yes	600
WI-26-20							yes	600
WI-26-21							yes	600
WI-26-22							yes	600
WI-26-23							yes	600
WI-26-24							yes	600
WI-26-25							yes	600
WI-26-26							yes	600
WI-26-27							yes	600
WI-26-28							yes	600
WI-26-29							yes	600
WI-26-30							yes	600
WI-26-31							yes	600
WI-26-32							yes	600
WI-26-33							yes	600
WI-26-34							yes	600
WI-26-35							yes	600
WI-26-36							yes	600
WI-26-37							yes	600
WI-26-38							yes	600
WI-26-39							yes	600
WI-26-40							yes	600
WI-26-41							yes	600
WI-26-42							yes	600
WI-26-43							yes	600
WI-26-44							yes	600
WI-26-45							yes	600
WI-26-46							yes	600
WI-26-47							yes	600
WI-26-48							yes	600
WI-26-49							yes	600
WI-26-50							yes	600
WI-26-51							yes	600
WI-26-52							yes	600
WI-26-53							yes	600
WI-26-54							yes	600
WI-26-55							yes	600
WI-26-56							yes	600
WI-26-57							yes	600
WI-26-58							yes	600
WI-26-59							yes	600
WI-26-60							yes	600
WI-26-61							yes	600
WI-26-62							yes	600
WI-26-63							yes	600
WI-26-64							yes	600
WI-26-65							yes	600
WI-26-66							yes	600
WI-26-67							yes	600
WI-26-68							yes	600
WI-26-69							yes	600
WI-26-70							yes	600
WI-26-71							yes	600
WI-26-72							yes	600
WI-26-73							yes	600
WI-26-74							yes	600
WI-26-75							yes	600
WI-26-76							yes	600
WI-26-77							yes	600
WI-26-78							yes	600
WI-26-79							yes	600
WI-26-80							yes	600
WI-26-81							yes	600
WI-26-82							yes	600
WI-26-83							yes	600
WI-26-84							yes	600
WI-26-85							yes	600
WI-26-86							yes	600
WI-26-87							yes	600
WI-26-88							yes	600
WI-26-89							yes	600
WI-26-90							yes	600
WI-26-91							yes	600
WI-26-92							yes	600
WI-26-93							yes	600
WI-26-94							yes	600
WI-26-95							yes	600
WI-26-96							yes	600
WI-26-97							yes	600
WI-26-98							yes	600
WI-26-99							yes	600
WI-26-100							yes	600

WEST

Table 4

Gene Name	SP ID#	na ID#	aa	Family	Group	Length, AA	Extra-Catalytic Domains (Amino acid positions)
X69117_h_beta_adrenergic	H	1	122	AGC	GRK	688	Regulator of G protein signaling domain 54-175; PH domain 559-652
AA144574_m	M	2	123	AGC	GRK	378	PH domain 249-337
AA210825_h	H	9	130	AGC	PKC	978	Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577
AA316804_h	H	11	132	AGC	PKC	890	Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532
AA387783_h	H	21	142	AGC	SGK	446	PX domain 13-120
AA021445_h_3	H	32	152	CAMK	EMK	1311	Vitamin K-dependent carboxylase/panama-carboxylutamic (GLA) domain 1072-1113
R31237_1_h_AAC3348	H	34	154	CAMK	EMK	729	UBA domain 327-365
408786.5_h	H	38	158	CAMK	EMK	1330	PAS domain 133-186, 247-280, 354-386
Z38720_h	H	41	181	CAMK	MLCK	874	WD domain, G-beta repeat 674-711
SGK088_h	H	42	182	CAMK	Trk	2287	Immunoglobulin domain 1-82, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-350, 1697-1779
R19772_h	H	44	184	CAMK	Trk	1287	RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain 419-528
17000138801197_h_IRA	H	76	195	Other	IRAK	598	Death domain 26-108
AA088547_h	H	78	197	Other	IRE	922	PQQ enzyme repeat 39-76
AA232253_h	H	82	201	Other	MLK	800	SAM domain (Sterile alpha motif) 337-408
AA599286_h	H	80	208	Other	SLOB	649	PX domain 16-122
AA836348_h	H	113	232	STE	NEK	838	Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650
PAK6_h	H	115	234	STE	STE20-02	719	P21-Rho-binding domain 11-69

FIGURE 1A

SEQ ID NO: 122_X69117_H BARK2_H

MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN
 QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC
 SHPFSKQAVEHVQSHLSKKQVTSTLFPYIEBICESLRGDI FQKFMESDKFTRFCQWKNV
 ELNIHLTMNEFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLDKKRIKMKQGETLALNER
 IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVSSEKEMRFYATE
 IILGLEHVHNRFFVYRDLKPANILLDEHGHAIRISDLGLACDFS KKKPHASVGTHGYMAPE
 VLQKGTAYDSSADWFSLGCMFLKLLRGHSPFRQHKTCDKHEIDRMTLTNVNVELPDTFSPE
 LKSLLEGLLQRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHLYLQKYPPLIPPRGEVNAA
 DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTETVYEAVNADTDKIEARK
 RAKNKQLGHEEDYALGKDCIMHGYMLKLGPNFLTQWQRRYFYLFNRLWRGEGESRQNL
 LTMEQILSVEETQIKDKKCILFRIGKGKQFVLQCESDPEFVQWKKEINETFKEAQRLLRR
 APKFLNKPRSGTVELPKPSLCHRNNSGL

SEQ ID NO: 123_AA144574_M BARK2_M

CFVVYRDLKPANILLDEYGHVRIISDLGLACDFS KKKPHASVGTHGYMAPEVLQKGTCTYDS
 SADWFSLGCMFLKLLRGHSPFRQHKTCDKHEIDRMTLTNVNQLPDAFSPELRSLEGLLQ
 RDVSQRLGCGGGGARELKEHIFFKGIDWQHLYLRKYPPPLIPPRGEVNAAADAFDIGSFDE
 EDTKGIKLLDCDQDLYKNFPLVISERWQQEVVETIYDAVNADTDKIEARKKAKNKQLGQE
 EDYAMGKDCIMHGYMLKLGPNFLTQWQRRYFYLFNRLWRGEGESRQSLTMEQIMSVE
 ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPR
 AILEFSKPPLCHRNSSGL

SEQ ID NO: 124_AA826850_H

MGSSMSAATARRPVFDDKEDVNFDFHFIILRAIGKGSFGKVCIVQKRDTEKMYAMKYMKNQ
 QCIERDEVNRNVFRELEILQEIHEVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQONVQ
 FSEDTVRLYICEMALALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNIATIIKDG
 TALAGTKPYMAPEIFXS FVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLV
 QLFSTVSVQYVPTWSKEMVALLRKLTLVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRV
 PGFVPNKGRHLCDPTFELEEMILESRLPHKKKKRLAKNKS RDNSRDSSQSENDYLQDCLD
 AIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125_AA960957_H

MGGNHSHPVPFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTEKMYAMKYMKNQKCI
 ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQONVHFT
 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHHITDFNIATVVKGAERASSM
 AGTKPYMAPEVFQVYMDRGPYSYPVDWWSLGITAYELLRGWRPYEIH SVTPIDEILNMF
 KVERVHYSSTWCKGMVALLRKLTKDPESRVSSLHDIQSVPYLADMNWDVAFKKALMPGF
 VPNGRLNCDPTFELEEMILESRLPHKKKKRLAKNKS RDGTDSCPLNGHLQHCLETVRE
 EFIIFNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNLLTHTCTRGCSS

SEQ ID NO: 126_TBK1_H

MQSTSNHLWLLSDILGQATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK
 KLNHKNIVKLFAIEEETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV
 GGMNHLRENGIVHRDIKPGNIMRVIGEDGQS VYKLTDFGAARELEDDEQFVS LYGTEEYL
 HPDMYERAVLRKDHQKKYGATVDLWSIGVTFFYHAATGSLPFRPFEGPRRNKEVMYKIITG
 KPSGAISGVQKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQFFA
 ETS DILHRMVIHVFSLQQMTAKHIYIHSYNTATIFHELVYKQTKIISSNQELIYEGRRLV
 LEPGRLAQHFPKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLGDASMAKAITG
 VVCYACRIASTLLLYQELMRKGIRWLIELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

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FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE
GTHPKDRNVEKLQVLLNCMTEIYYQFKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH
FTDECVKKYEAFLNKSEEWIRKMLHLRQQLSLTNQCFDIEEEVSKYQEYTNELQETLPQ
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMD
GGLRNVDCI

SEQ ID NO: 127_AA305176_H

MDPTAGSKKEPGGGAATEEGVNRIVPKPPSIEEFSIVKPISRGAFGKVYLQKGGKLYA
VKVVKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLSANNVYLVMEYLIGGDVKS
LLHIYGYFDEEMAVKYISEVALALDYLHRHGIHRDLKPDNMLISNEGHIKLTDFGLSKV
TLNRDINMMDILTTPSMAPRQDYSRTPGQVLSLISSLGNTPIAEKNQDPANILSACLS
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128_AA116841_M

TRPIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV
PQPDDDETDSYFEARNNAQHLTVSGFSL

SEQ ID NO: 129_AA256100_H

MAMTAGTTTTFPMNHTRERVTVAKLTLENFYSNLILQHEERETRQKKLEVAMEEEGLAD
EEKKLRRSQHARKETEFRLRLKRTLGLDDFESLKVIGRGAFGEVRLVQKKDTHIYAMKI
LRKSDMLEKEQVAHIRAERDILVEADGAWVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM
KKDTLTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLDAKGHVKLSDFGLCTGLKK
AHRTEFYRNLTNPPSDFSFQNMNSKRKAETWKKNRRLAYSTVGTPDYIAPEVFMQTGY
NKLCDWWSLGVIMYEMLIGYPPFCSETPQETYRKVMNWKETLVFPPEVPISEKAKDLILR
FCIDSENIRIGNSGVVEIKGHPFFEGVDWEHIRERPAAPIEIKSIDDTSNFDFFPESDIL
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQGRSIPITYMKAGKL

SEQ ID NO: 130_AA210825_H

DSLLPTPALGTPLPIWPVGSRLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG
SPLSHHLLTRSRGSRTOGPPGPPGSGSRVGSRRVAVPGLPPWPPPPHYAGLPGPSPPGSP
PPGGLQLQSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVQQLACSIVDQKF
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVLSASATFEDFQIRPHAL
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLNHYHKRCAFSIPNNCSGARKRRLSSTSL
ASGHSVRLGTSESPLCTAEELSRSTTELLPRPPSSSSSSSSASSYTGRPIELDKMLLSKV
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDCKFNCHKRCATRVNDCLGEALIN
GDVPMEEATDFSEADKSALMDESEDSGVI PGSHSENALHASEEEEEEGGKAQSSLYIPL
MRVVQSVRHTTRKSSTTLREGVWVHYSNKDTLRKRHYWRDLCKCITLFQNNTTNRYKBI
PLSEILTVEQAQNFSLVPPGTNPFCFEIVTANATYFVGEMPGGTPGGPSGQGAEAARGLX
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG
QFGVVYGGKHKRTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLRHPGIVNLECMFETP
EKVFVMEKLHGDMLEMILSSEKGRLPRLTKFLITQILVALRHLHFKNIVHCDLKPENV
LLASADFPFQVKLCDFGFARIIGEKSFRRSVVGTAYLAPEVLLNQGYNRSLDMWSVGVI
MYVSLSGTFFNEDEDINDQIQNAAFMYPASPSHISAGAIIDLINNLLQVKMRKRYSDK
SLSHFWLQEQYQWLDLRELEGKMGERYITHESDDARWEQFAAEHPLPGSGLPPTDRDLGGA
CPPQDHDMMQGLAERISVL

SEQ ID NO: 131_AA127299_H

IQFIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKTLTPTWNETFFVHFPEKTTLEL
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

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FIGURE 1C

SEQ ID NO: 132_AA316804_H

MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV
SFLQLIGLTRSVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN
ILQLITSADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR
QQLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLOPEYVALPSEES
HVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSRSSRGLDDT
EPPSPPEDKMFLLDPSDLVERDEEAVKTISPSTSNNIPLMRVVQSIKHTKRKSSTMVKE
GWMVHYTSRDNLKRHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG
SNPHCFEIIITDMVYFVGENNGDSSHPVLAATGVGLDVAQSWEKAIRQALMPVTPQASV
CTSPGQGDHKLSTSSISVSNCCIENVDISTVYQIFADEVLGSGQFGIVYGGKHKRTGR
DVAIKVIDKMRFPKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFFVMEKLHGDM
EMILSSEKSRLEPITKFMVTQILVALRNLHFKNIVHCDLKPENVLASAEPFPQVKLCD
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSGYNRSLDMWSVGVIYVSLSGTFPFNEDE
DINDQIQNAAFMYPPNPWREISGEAIDLINLLQVKMRKRYSDKSLSHPWLDQYQTLWD
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133_PKNBETA_H

MEEGAPRQPGPSQWPPPEDEKEVIRRAIQELKIKEGVENLRRVATDRRHGLGHVQQLLRSS
NRRLEQLHRELHARILLPGPGPGAEPVASGPRPWAEQLRARHLEALRRQLHVELKV
KQGAENMTHTCASGTPKERKLLAAQQLRDSQLKVALLRMKISSLEASGSPEPGPELLA
EELQHRHLHVEAAVAEGAKNVVLLSSRRTQDRKALAEAAQLQESSQKLDLLRLALEQLL
EQLPPAHLRSRVTRERAAVPGYPQPSGTPVKPTALTGTQLQVRLGCEQLLTAVPGRSP
AAALASSPSEGWLRTAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI
PLERARELEIGVHWRDWRQLCGVAFLRLEDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSSPSTISPPKGCPR
PTTLREASDPATPSNPLPKTPLGEEMTPPKPPRLYLPEPTSEETPRTKRPHMEPRTR
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLLVQFKGTGKYAIAKALKKQEVLSRDE
IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSSHARFVTEFVPGGDLMMQIHEDVFPEPQ
ARFYVACVVLGLQFLHEKKIIYRDLKLDNLLDAQGFLKIADFGLCKEGIGFGDRTSTFC
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPG
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFFRTTNWQALLARTIQPPFVPTLC
GPADLRYFEGEFTGLPPALTTPPAPHSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 134_AI021023_M_PKNBETA_M

LKWDNLLLLDAQGFLKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG
LGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA
GEQDAEEIKVQPPFFRTTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTTPPAP
HSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 135_H19102_H

GGNIRGPWARGWKSJWTGLTIRSDLEELWELRGHHYHQLHESLKPAPVLVEKPLPEWPVP
QFINLFLPEFPPIRPIRGQQQLKILGLVAKGSFGTVLVLDCTQKAVFAVKVVPKVKVLQR
DTVROCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYSTDLYSLWSAVGCFPEASI
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHAAMLASVTHSDSEIPAS
LNQGLSLLLHELLCQNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS
SAETMPFDDFDCDLESFLLYPIPA

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FIGURE 1D

SEQ ID NO: 136_AA476563_H

MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFTLPDGDSASRSFNTSESKVEFKAQ
DTISRGSDSDSVFVIFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN
IGIENKLLEAPDVLCLRLSTEQCQAHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF
VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTEESLFRICSPLSGANEYIASTDT
LKTEEVLLFTDQTDLLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS
CSDSAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP
ECVSEEARSLIQQLQFNPLERLGAGVAGVEDIKSHPFFTPVDWAEMLR

SEQ ID NO: 137_AA626690_H

MLPFAPQDEPWDREMEVFSGGGASSGEVNLKMOVDEPMEEGEADSCHDEGVVKEIPITHH
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT
KMERDILVEVNHPPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTEEDVKFYLA
ELALALDHLHQLGIVYRDLKPENILLDEIGHIKLTDGFLSKESVDQEKKAYSFCGTVEYM
APEVNVNRRGHSQSADWWSYGVLMEMLTGTLPFQKGKDRNETMNMILKAKLGMPQFLSAEA
QSLRLMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDFTCF
DPEFTAKTPKDSPLPASANAHQLFKGFSFVATSIAEYKITPITSANVLPVQINGNAA
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI
ITLKDVFDDGRYVYLVTDLMKGGEILLDRILKQKCFEREASDILYVISKTVDYLHCQGVV
HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGLLLTPCYTANFVAPEVLMQOGYD
AACDIWSLGLVLYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKAMVATYSALTHKTFQ
PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138_AA215680_H

MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPMTKRDYLVDAATQIRLA
LERDVSEDEYAAFNHYQNGVDVLLRGIHVDPNKERREAVKLKITKYLRRAEIEFNCHLQR
PLSSGASPSAGFSSLRLRPITLSSAVEQLRGCRVVGVIKVLVQDPATGGTFVVKSLP
RCHMVSRLRTIIPHGVPMYTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL
SSGSTQERMKAQLNPHLNLTPARLPSGHAPGDRIALEPPRTSPNLLLAGAPSTRPQR
BAEGEPTARTSTSGSSDLPKAPCGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG
RGMDQSCLSADGAGRGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLPNGLLL
DQAGHIRLTYFGQWSEVEPQCCGEAVDNLYSAPEVGGISELTEACDWWSFGLLYELLTG
MALSQSHPSGIIQAHTQLQLPEWLSRPAASLLTELLQFEPTRRLLGMGEGGVSKLKSHPPFS
TIQWSKLVG

SEQ ID NO: 139_SGK_H

MTVKTEAAKGTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKI
SQPQPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA
EVFYAVKVLQKKAILKKKEEKHIMSENVLLKNVHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSR
NTAEMYDNILNKPLQLKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW
DDLKINKITPPFNPVSGPNELRHFDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFLG
FSYAPPTDSFL

SEQ ID NO: 140_AA107515_M

MTVKAEAAARSTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM
SHPQPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA

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FIGURE 1E

EVFYAVKVLQKKAILKKKKEKHIMSERNVLLKNVHKPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN
TAEMYDNILNKPLQKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD
DLINKKITPPFNPVSGPSDLRHFDPFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF
SYAPPVDSFL

SEQ ID NO: 141_AA109508_M

HLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGLCKE
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVSQMY
ENILHQPLQIPGGRTVAACDLLQSLHKKDQRLGSKADFLEIKNHVFFSPINWDDLYHK
RLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD
ILDC

SEQ ID NO: 142_AA887783_H

MQRDHTMDYKESCPVXIPSSDEHREKKKRFTVYKVLVSVGRSEWVFVRRYAEDKLYNT
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMD
SPKHQSDPSEDEDERSSQKLHSTSQNINLGPSPGNPHAKPTDFDFLKVIGKGSFGKVLLAK
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVHKPFLVGLHYSFOTTEKLYFVL
DFVNGGEGHVLTDFGLCKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTVDWWCLGAV
LYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWISILEELLEKDRQNRLGAKEDF
LEIQNHPPFESLSWADLVQKKIPPPFNPVAGPDDIRNFDATFTEETVPYSVCVSSDYSI
VNASVLEADDAFVGFSYAPPSDFL

SEQ ID NO: 143_R47805_H

MAHQGTGIHATEELKEFFAKARAGSVRLIKVVIEDEQLVLGASQEPVGRWDQDYDRAVLPL
LDAQQPCYLLYRLDSQNAQGFEWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDE
LFGTVKDDLSFAGYQKHLSSCAAPPLTSAERELQQIRINEVKTEISVESKHQTLQGLAF
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL
YKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLDSVEQDFHLEIAKKIEIGDG
AELTAFLYDEVHPKQHAFKQAFAPKPGPGGKRGHKRLIRGPGENGDD

SEQ ID NO: 144_H60215_H

MSKLRMKRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR
KDGTDFFYQLKILTLEERGQDQIESQEERQGMILLHTEYSLLSLLHTQDGVVHHHGLFQD
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV
VIFYDVVRVVEALHQKNIVHRDLKLGNMVNLKRTHRITITNFCGLGHLVSEGDLKQDQRG
SPAYISPDVLSGRPYRGKPSDMWALGVVLFMTLYGQFPFYDSIPQELFRKIKAAEYTIPE
DGRVSENTVCLIRKLLVLDPPQRLAAADVLEALSALIASWQSLSSLSGPLQVVPDIDDQM
SNADSSQEAKVTEECSEQYEFENYMRQQLLLAEKSSIHDTRSWVPKRQFGSAPPVRRGLH
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145_SGK324_H

MASTRSIELEHFEERDKRPRPGSRRGAPSSSSGGSSSSSGPKGNGLIPSPAHSACSFYRTR
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV
RTIYITIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGTSRALAAA
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKTAHSFEQVLTIDITEAIKXASG
VVKRLCTLDGKQVRVTCVHLPDFFGDDDFIACGPEKFRYAQDDFVLDHSECRVLKSSYS
RSSAVKYSGSKSPGPSRRSQISAHGRSSSNVNGGPELDRCSPEGVNGNRCSESSTLLEK
YKIGKVIKVGDNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

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FIGURE 1F

MLVEEMETATEFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH
 RDIKPENLLVCEYPDGTSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD
 IWAAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ
 VNVEARCTAGQILSHPWVSDDASQENMQAEVTGKLKQHFNNALPKQNSTTTGVSVMVS
 GRRQVWPCGAGLEVFEFGSRELPSHGSWCLP

SEQ ID NO: 146_W30246_M SGK324_M
 TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPGVNGNRCSESFPILLEKYR
 IGKVIDGDNFAVVKECVDRTYGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNIIML
 VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHLSLSIVHRD
 IKPENLLVCEYPDGTSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW
 AAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPVCVFRKCL

SEQ ID NO: 147_AA383293_H
 PAAKRVVYRNGDPFFPGSQLVVTQRRFPTMEAFLECVTSQAPLAVRALYTPCHGHPV
 TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPFSLKLSQAASQDWETVL
 KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPPALSTRGLLAA
 GNEAHLRSGVGTVAGSPKPLGRKAKKETCLIVTLTLKYQQSETSRDQGSFPGSVIGVYGA
 PHRRKETAGALEVADDEDQTTEEPDQRAAQIVEQVTCLODFGDDDDVFIACGPEKFRYA
 QDDFVLDHSRRRLREHQAGFEKLRRTGEEKEAEKEKKPCMSGRRMTLRDDQPAKLEK
 EPKTRPEENKPERPSGRKPRPMGIIAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYA
 MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI
 IESVKFPEPDAALMIMDLCKALVHMDKSIVHRDLKPENLLVQRNEDKSTTLKLADFGLA
 KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPXXGDQDE
 LFNIIQLGHFEFLPPYWDNISDAAKDLVSRLLVDPKKRYTAHQVLQHPWIETAGKTNTV
 KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148_AA197883_M
 MPTAPVLRPPPPATPAPPAPSRPAPPPIGHRGPCDHSLKCLSSKISERKLPGPWLPAGR
 GPLEKPVLGPRGAVMPLFSPQSSLSHVSRAEHSPLKPRVTVVKLGQPLRKATLLNRRS
 VQTFEQLLSDISEALGFPRWKNDVRKLFTLKGREVKSVSDFFREGDAFIAMGKEPLTLK
 SIQLAMEELYPKNRALALAPHSRVPSRLRSRLPSKLLKGSHRCGEAGSYSAEMESKAVS
 RHQGTSTVLAPEDKARAQKWVRGKQSESEPGGPPSPGAATQEETHASGEKHLGVEIEKTS
 GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRRPSKAKFTD
 GEEGWKGDShrgsPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQGAPKAQKDFVEGPPAV
 EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPLPRTRGEEKQAEHEKKPGGLGERRAPE
 KESKRKLEEKRPERPSGRKPRPKGIIISADVEKHYDIGGVIGDGNFATVKECRHRETRQAY
 AMKMIDKSQKKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA
 IVENVKFPEPEAAVMITDLCKAFVHMDKNIVHRDVKPENLLVQRNEDKSTTLKLADFGLA
 AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPERDQDE
 LFNIIQVGQFEFLSPYWDNISDAAKDLVRNLLVEDPKKRYTAEQVLQHPWIEMVGHNTG
 NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149_DRAK2_H
 MSRRRFDRCRSISGLLTTPQIPIKMENFNNFYILTSKELGRGKFAVVRQCISKSTGQEYA
 AKFLKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS
 LCLPELAEMVSENDVIRLIKQILEGVYYLHQNNIVHLDLKPQNILLSSYPLGDIKIVDF
 GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
 QETYNLISQVNVVDYSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSLWQQWDFEN

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FIGURE 1G

LFHPEETSSSSQTQDHSVRSSDKTSKSSCNGTCGDREDKENIPEDSSMVSKRFRFDDSL
PNPHELVSDDLCC

SEQ ID NO: 150_W44160_M_DRAK2_M

MSRRRFDCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA
AKSLKKRRRGQDCRAEILHEIAVLELARSCHVINLHEVYENATEIILVLEYAAGGEIFN
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNINIVHLDLKPQNILLSSIIYPLGDIKIVDF
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYNISQVNVVDYSEEMFSSVSQATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENIPEDGSLVSKRFRFDDSL
PSPHELVPDLFC

SEQ ID NO: 151_H01248_H, DRAK1_H

MIPLEKPGSGGSSPGATSGSGRAGRLSGPCRPPPPPPQARGLLTEIRAVVRTEPFQDGY
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEIIHEIAVLELAQDNPW
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR
DVVHLDLKPQNILLTSESPLGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI
SMATDMWSIGVLTYVMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSESAVIDFIRT
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDTDKSE
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAISKRFKFEEPLLQEIPGEFIY

SEQ ID NO: 152_AA021445_H

MPARIGYYEIDRTIGKGNFAVVKRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF
CHCRNIVHRDLKAENLLLDANLNIAIDFGFSNLFPTGQLLKTWCGSPPYAAPELFEGKE
YDGPKVDIWSLGVVLYVLVCGALPFDGSTLQNLRARVLSGKFRIFFMSTECEHLIRHML
VLDPNKRLSMEQICKHKWMKLGADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL
DKEQTLQSLRSDAYDHYSIAIYSLCDRHKRKTLLRLGALPSMPRALAFQAPVNIQAEQAG
TAMNISVPQVQLINPENQIVEPDGTLNLDSDGEPEPSPEALVRYLSMRRTVGVADPRTE
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNLPMQNLQPTGQLEYKEQSLLQPPTLQ
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPOQ
EAVQRYLANRSKRHTLAMTNPTAEIPDLQRLGQQPFRSRVWPPHLVPDQHRSTYKDSN
TLHLPTERFSPVRRFSDGAASIQAFKAHLEKMGNNSSIKQLQCECEQLQKMYGGQIDERT
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQSPPLQAACENQPALLTHQLRLRIQPS
SPPPNHNPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQFENCSSPPN
VALTCLGMQQAQSQQVTIQVQEPVDMLSNMPGTAAGSSSGRGISISPSAGQMOMQHRTNL
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYDQAHLPPLFSDQSRGSPSSYSPST
GVGFSPTQALKVPPLDQFPFTFPPSAHQPPPHYTTALQQLSPTPPDYTRHQVPHILO
GLLSPRHSLTGHSIDIRLPPTFAQLIKRQQQQRQQQQQQQQQEQYQELFRHMNQGDAGSL
APSLGGQSMTERQALSQNADSYHHHTSPQHLLQIRAEQCVSQASSPTPPHGYAHQPALM
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG
IHPYGHQPTAAFSKNKVPSPREPVIGNCMRDSPPGQAVELPDHNGLGYPARPSVHEHHRPR
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE
CGASLGGHEHPDLSDGSQHLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153_2R22-5-11_H

MTAVYMNNGGLVNPYARWDRRDSVESGCQTESSKEGEGQPRQLTPFEKLTQDMSQDEK
VVREITLGRIGFYRIRGEIGSGNFSQVKLGIHSLTKEKVAIKILDKTKLDQKTQRLLSR
EISSMEKLHHPNIIIRLYEVVETLSKLHLVMEYAGGGELFGKISTEGKLEPESKLIFSQI
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

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FIGURE 1H

LFRDEHYIGIYVDI WALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR
LIRGVLQQIPTERYGIDCIMNDEWMQGVPTPLEPFQLDPKHLSETSTLKEEENEVKST
LEHLGITTEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPVMMPLDPKERDLKKGS
RVYRGIRHTSKFCSIL

SEQ ID NO: 154_R31237_1_H, AAC33487
MSTRTPLPVNERDTENHTSHGDGRQEVTSRTSRSGARCRNSIASCADQPHIGNYRLK
TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLQKLFREVRIMKILNHPNIVKLFE
VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK
AENLLLDADMNIKIADFGFSNEFTVGGKLDTF CGSPPYAAPELFQGGKYDGPEVDVWSLG
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRGTLQ
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT
YLLGRKSSELDASDSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQSVSSSQKQRRYSD
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPMLGNASNPKN
ADIPERKKSSTVPSSNTASGGMTRNTYVCSERTTADRHSVIQNGKENSTIPDQRTPVAS
THSISSAATPDRI RFPRTASRSTFHGQPRERTATYNGPPASPSLSHEATPLSQTRSRG
STNLF SKLTSKLTRSRNVSAEQDENKEAKPRSLRFTWSMKTTSMDPGDMMREIRKVL D
ANNCDYBQRRERFLFCVHGDGHAENLVQWEMEVC KLPRLSLNGVRFKRISGTSIAFKNIA
SKIANELKL

SEQ ID NO: 155_W90839_M
KGPSWSSRSLGARCRNSIASCPEEQPHVGNRYLLRTIGKGNFAKVKLARHILTGREVAIK
IIDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIETEKTLYLIMEYASAGEVFDYLV
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLDAAENIKIADFGFSNEFTL
GSKLDTF CGSPPYAAPELFQGGKYDGPEVDIWSLGVILYTLVSGSLPFDGHNKELRERV
LRGKYRVFPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE
RMPGRKASCSAVGSGSRGLPPSSPMVSSAHNPNAEIPERRKDSTSTPNLPPSMMTRRN
TYVCTERPGSERPSLLPNGKENS SGT SRVPPASPSHSLAPPSGERSRLARGSTIRSTFH
GGQVRDRRAGSGSGGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLT SKLTRRV TDE
PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156_406786.5_H
MEVGGLTVFEEDQRCLSQLPLPVS AEGPAAQT TAEP SRSFSSAHRHLSRRNGLSRLCQS
RTALSEDRWSSYCLSSLA AQNIC TSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS
PLLPA PVCNPNAI FTVD AKTTEILVANDKACGLLGYSQDLIGQKLTQFFLRSDSDVVE
ALSEE HMEADGHAAVFGTVVDIITRSGEKIPVSVWMKMRQERRLC CVVLEPVERVST
WVAFQSDGTITSCDSLFAHLHGYVSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIORSV
GRARDGTTFFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI
NHSFALTFLFGYKTELLGKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDVGNESGGER
TLDPWQGGQDPAEGGQDPRINVVL AGGHVVP RDEIRKLME SQDIFTGTQTELIAGGQLLSC
LSPQAPAGVDNVPEGSLPVHGEQALPKDQQTALGREEPVAIESPGQDLLGESRSEPVDV
KPFASCEDSEAPVPAEDGGS DAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ
LAGGSLLMHCPCYGEWGLWWR SQDLAPSPSGMAGLSFGTPTLDEPWLG VENDORREELQTC
LIKEQLS QLSLAGALDVPHAE LVPTECQAVTAPVSSCDLGGRDL CGGCTGSSSACYALAT
DLPGGLEAVEAQEVDVNSFSWNLKELFFSDQTDQTSSNCSCATSELRETPSSLAVGSDPD
VGS LQEQGSCVLD DRELLLLLTGTCVDLGQRRRFRESCVGHDPTEPLEVCLVSSEHYAASD
RESPGHVPSTLDAGPEDT CPSAE EPRLN VQVTSTPVI VMRGAAGLQREIQEGAYSGSCYH
RDGLRLSIQFEVRRVELQGPTPLFCCWL VKDLLHSQRDSAARTRLFLASLPGSTHSTAAE
LTGPSLVEVLRARPWFEEPPKAVELEGLAACEGEYSQKYSTMSPLGSGAFGVWTAVDKG
KNKEVVVKFIKKEKVLEDCWIEDPKLGKVLTLEIAILSRVEHANI IKVLDIFENQGFQVL

FIGURE 11

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDIHRDIKDEN
IVIAEDFTIKLIDFGSAAYLERGKLFYTFCTIEYCAPEVLMGNPYRGPELEMWSLGVTL
YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVTDWPVWTO
PVNLADYTWEEVFRVKNPESGVLSAASLEMGNRSLSVAQAQELCGGPVPGEPNGQGCL
HPGDPRLTTS

SEQ ID NO: 157_AA544838_M 406786_M

TRPHPCLEPLASFIFRQLVSAVGYLHSQGIHRDIKDENIVIAEDFTIKLIDFGSAAYL
ERGKLFYTFCTIEYCAPEVLIGNPYRGPELEMWSLGVTLTYTLIFEENPFCEVEETMEAV
IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLVIRDPWVTQPVNLASYTWEEVCRTNQPS
GLLSAASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPPLPVS

SEQ ID NO: 158_AA785735_H

MVMADGPRHLQRGPVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDSQLDVN
LEKIYREVQIMKMLDHPHIIKLYQVMETKSMYLVTEYAKNGEIFDYLANHGRNNESEAR
RKFWQILSAVDYCHGRKIVHRDLKAENLLDNNMNIKIADFGFGNFFKSGELLATWCGSP
PYAAPEVFEGQQYEGPQLDIWSMGVVLVYLVCGALPFDGPTLPILRQRVLEGRFRIPIYFM
SEDCEHLIRMLVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV
LRLMHSGLIDQKXIESLONKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
AEQTVAKAQTVGLPVTMHSNMRLLRSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT
PKVNGCLLDPPVPLVRKGCQSLPSNMMETSIDEGLETEGEAEEDPAHAFAEFQSTRSGQ
RRHTLSEVTNQLVMPGAGKIFSMNDSPLSDSDSEYDMGVSQVDLNFLEDNPSLKDIML
ANQPSPRMTSPFISLRPTNPAMQALSSQKREVNHRSPVSFREGRRASDTSLTQGVAFRQ
HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
LPASVHPQLSPROSLETQYLQHRLOKPSLLSKAQNTCQLYCKEPPRSLEQQQLQEHRLQOK
RLFLQKQSQLQAYFNQMQUIAESSYPQPSQQPLPRQETPPPSQQAPPFSLTQPLSPVLEP
SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPA
PLQFSYQTCELPASAASPAPDYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLAL
SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159_AA207220_H

MESLVFARRSGTPSAEELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRRHYEFLETG
KGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIEHVEFE
NSSKIVIVMEYASRGDLYDIYSERQQLSREARHFFRQIVSAVHYCHQNRVVRDLKLEN
ILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSLGVLL
YILVHGTMFPDGHDKILVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS
HWWVNWGYATRVGEQEPHEGGHPGSDSARASMADWLRRSSRPLENGAKVCSFFKQHAP
GGGSTTPGLERQHSLSKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPGKILKKKVSASA
EGVQEDPPELSPIPASPGQAAPLLPKKGIKKPRQRESGYYSPEPSESSELDDAGDVVF
SGDPKEQKPPQASGLLLHRKGILKLNKFSQTALELAAPTTFGSLDELAPPRPLARASRP
SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSDNLTGLEEPPSEGPGLSCLRRWRQDP
LGDSCFSLTDCQEVATATYRQALRVCSKLT

SEQ ID NO: 160_AA426580_H, MAK_V_H

MPAAAGDGLLGEPAAPGGGGGAEDAARPAACEGSFLPAWVSGVPRERLRDFQHHKRVGN
YLIGSRKLGEFSFAKVREGLHVLTEKVAIKVIDKKRAKDDTYVTKNLRREGQIQQMIRH
PNITQLLDILETENSYYLMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA
GVVHRDLKIENLLLEDNNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY
GPKIDVWSIGVNMAYMLTGTLPTVEPFSLRALYQKMDKEMNPLPTQLSTGAISFLRSL
LEPDPVKRPNIQQALANRWLNENYTGKVPNCVTPNRI SLEDLSPSVVLHMTKELGYKNS

FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCKYKTRLYQIEKYRAPKESYEA
 SLDTWTRDLEFHAVQDKKPKKEQEKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA
 LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNVASSSMEFIPVPPPRTPRIVKKPEPHQP
 GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS
 PGLPSGMSPLHTPLHPTLVSFHEDKNSPPKEEGLCCPPPVPSNGPMQPLGSPNCVKSR
 GRFPMGIGQMLRKRHQSLSQPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161_Z36720_H

MDTKLNMLNEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI
 DTQAGWPEVLELVRAMQQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG
 RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQDKGELSAEQGIWATLMTLV
 IMVTAANKERVEEEGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIRASGLG
 ADPAQAVVSPGQGDGVPGPAQAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAGRVNV
 VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTPGPGPQCPGPPGLPAQARATHSGGETPP
 RAALLKGAVAPGFSRRDLVFPISIFCACLGISIHQEMDTPGEMLMTGRGSLGPTLTTEAP
 AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEEQRAGAEPG
 TRPSLARSDNDHEVGALGLQOGKSPGAGNPEPEQDCAARAPVRAEAVRRMPGAEAGSV
 VLDDSPAPPAPFEHRVSVKETSISAGYEVQCHEVLGGGRFGQVHRCTEKSTGLPLAAKI
 IKVKSADREDVKNEINIMNQLSHVNLILQLYDAFESKHSTLVMYVDGGELFDRITDEK
 YHLTELDVVLFTROIPEGVHYLHQHYILHLDLKPENILCVNQTGHQIKIIDFGLARRYKP
 REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLLSGLSPFLGETDAETMNFIV
 NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNNLPAKASRSKTRLK
 SQLLLQKYIAQRKWKKHFYVVTAAANRLRKFPPTSP

SEQ ID NO: 162_SGK088_H

GEMALFECLVAGPTDVEVDWLCRGRLLQPALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC
 KLSTAKDELTCARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFG
 CPMEESENLRLRQDGGHLSLHIAHVGESEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAAS
 GPSSKLEKMPISIPPEEQGELERLSIPDFLRPLQDLEVLGLAKEAMLECQVTGLPYPTISW
 FHNGHRIQSSDDRRMTQYRDVHRLVFPVAVGPOHAGVYKSVIANKLKGAACYAHLVYTDVV
 PGPPDGAPQVAVTGRMVTLTWNPPRSILMAIDPDSLTYTVQHQLGSDQWTALVTGLRE
 PGWAATGLRKGVQHIFRVLSTTVKSSSKSPSPSEPVLLEHGPTLEEAPAMLDKPDIVYV
 VEGQPASVTVTFNHVEAQVWVWSCRGALLEARAGVYELSOPDDQYCLRICRVSRDMDGA
 LTCTARNRHGTQTCVTELEAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD
 EVLLTSSHSVSFVYEENECSLVVLSTGAQDGGVYTCTAQNLAGEVSCKAELAVHSAQTAM
 EVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFIPSOAKPKAS
 ARREARLLARLQHDCVLYFHEAFERRRGLVIVTELCTEELLERIAKPTVCESEIRAYMR
 QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRI CDFGNAQELTPGEPQYCQYGT
 EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFGENDRTTLMNIRYNVAFETTF
 LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKFLSRRRWORSQ
 ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEELEELPSVPRPQOP
 EFGSRVSLTDIPTEDALGTPETGAATPMDWQEQGRAPSQDQEAPEALPSPGQEPAA
 GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG
 EYAQRLQALRQRLLRGGPEDGKVSGLRGPLLES LGGRARDPRMARAASSEAAPHHQPPE
 NRGLQKSSSFSQGEAEPRGRHRRAGAPLEIPVARLGARRLOESPSLSALSEAQPSSPARP
 SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVRAKPPAPPQALQTLALP
 LTPYAQIIQSLQLSGHAQGPSQGAAPPSEP KPHA AVFARVASPPPGAPEKRVPSAGGPP
 VLAEKARVPTVPPRPGSSSLSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG
 PFRGAEEEDGIYRPSAGTPELVRRPERSRSVQDLRAVGEPGLVRRLLSLSLQRLRRT
 PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQRS GSSSEDSSGGAS

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FIGURE 1K

GRSTPLFGRLRRATSEGESLRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES
 RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPFVFIHKLKDQVLLEGEAA
 TLLCLPAACPAPHISWMKDKKSLRSEPSVIVSCKDGRQLLSIPRAGKRHAGLYECSATN
 VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW
 HPVSSGIPDCYYNVTHLPVGVTVRFRVACANRAGQGPFSSNSSEKVFVRGTQDSSAVPSAA
 HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSSLKAVGPP
 PQTPRRHRGLQAARPAEPTLPSTHVTTPSEPFPVLDGTGPIIPASTPQGVKPVSSSTPVY
 VVTSFVSAPPAPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP
 PQKPYTFLEEKARGFRGVVRACRENATGRTFVAKIVPYAAEGKPRVLQYEYEVRLTLHHER
 IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMVQLLQGLDYLHGHV
 LHLDIKPDNLLLAPDNALKIVDFGSAQPNPQALRPLGHRTGTLEFMAPEMVKGEPIGSA
 TDIWGAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLSV
 HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLLR
 SYPGGP

SEQ ID NO: 163_AA542015_M SGK088_M

ATDIWGAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLS
 VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLL
 RSYPGSP

SEQ ID NO: 164_R19772_H

MKGDDRAYTRGPSLGWLFKACCCCFPCRDAYSHSSSENGGKSESANLQAQPSLNFHSS
 PGPKRSTNTLKKWLTSPVRRNLNSGKADGNIKKQKKVRDGRKSF DLGSPKPGDETTPQGDS
 ADESKKGWGEDEPDEESHTPLPPMKIFDNDPTQDEMSSSLAARQASTEVP TAADLVNA
 IEKLVKNKLSLEGSSYRGS LKDPAGCLNEGMAPPTPPKNPEEEQKAKALGRMFVLNELV
 QTEKDYYKDLGIVVEGFMKRIEEKGVPEMDRGKDKIVFGNIHQIYDWHKDFFLAELEKCI
 QEQDRLAQLFIKHERKLIYVWYCNKPRSEYIVAEYDAYFEEVKQEIINQRLTSLDFLIK
 PIQRITKYQLLLKDFLRYSEKAGLECS DIEKAVELMCLVPKRCNDMMNLGR LQGFEGTLT
 AQGKLLQDFTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGS LTPGYMFKRSIKMN
 YLVLEENVNDNDPCKFALMNRETSE RVVLQANADIQAWVQDINQVLETQDFLNALQSP
 IEYQKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPLPLPKISTSN GSP
 GFEYHQPGDKFEASKNDLGGCNGTSSMAV IKDYALKENEICVSQGEVVQVLAVNQNM C
 LVYQPASDHS PAAEGWVPGS ILAPLTKATAAESDGS IKKSCSWHTLRMRKRAEVENTG K
 NEATGPRPKPDILGNKVS VKETNSSESECDLDPNTSMEILNPNFIQEVAP EFLVPLVD
 VTCLLGDVTILQCKVCGRPKPTITWKGP DQNILDTDNSSATYTVSSCD SGEITLKI CNLM
 PQDSGIYTCIATNDHGTST SATVKVQGVPAAPNRPIAQERSCTSVILRWLP PSSTGNCT
 ISGYTVEYREEGSQIWQOSVASTLD TYLVIEDLSPGCPYQFRVSASN PWGISLPSEPSEF
 VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATRKDVAVKFVNKKM
 KKKEQAHEAALLQHLQHPQYITLHD TYESPTS YILILELMDDGRLLDYL MNHDELMEEK
 VAFYIRDIMEALQYLNCRVAHLDIK PENLLIDLRI PVPRVKLIDLEDAVQISGHFHIH H
 LLGNPEFAAPEVIQIPVSLGTDIWSIGV LTYVMLSGVSPFLDESKEETCINVC RVDFS F
 PHEYFCGVSNAA RDFINVILQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI
 ERRKHQNDVRPIPNVKS YIVNRVNQGT

SEQ ID NO: 165_5R72_8_2_H

MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLV VEMSQTSSIGSAESLISLERK
 KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEE IYTFGR
 ILGKGSFGIVIEATDKETETKWA IKKVNKEKAGSSAVKLLEREVNILKSVKHEHI IHLEQ
 VFETPKMYLVMELCEDGELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHRDLK
 LENIMVKSSLIDDNNEINLN IKTDFGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

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FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPPFLASSEAKLFELIRKGELHFENAVWNSISDCAKSVLKQ
LMKVDPAHRITAKELLDNQWLTGNKLSVRPTNVLEMMKEWKNNPESVEENTTEENKPS
TEEKLKSYQPWGNVPETNYTSDEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE
IKGEMEKTPVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166_SGK309_H

MQCLAAALKDETMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN
ALKVESAAQPKQVLKMEVAVLKKLQSGGLGQGDGKEEMKPGAKRGKDHVCRFIGCGRNE
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILEIEAHSVGLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYNTTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHD
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMKEKYEHRMLLKHPSEFHLFLDHIASLDY
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG
GQCDASAWGPAPGEHRGCATGRAPEXPGECTPNSAREALXGAGPQSPPCPPRGSXGXSL
GGDRCPQEQTPDQHRQSNCRQGEGRGWPFSLPPIPSLVPLPCSSXAPCPPPISLLARPLF
PVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167_AA234451_H

MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAAQPKQV
LKMEVAVLKKLQGDHVCFIGCGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTTISTTLR
LGRQILESIESIHSVGSXHRDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP
RAVAGFRGTVRYASINAHNRNREMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE
RYDHRLMLKHLPPFEISIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT
GNDGSLTTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP
VGVSPDKLPGSLGHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL
GSPIRVRSEITQPDRIPLVRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168_AA435956_H

TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSFQLFMFQLLRGLAYIHHQHVLHRDLKPQN
LLISHLGELKLADFGGLARAKSIPSQTYSSSEVVTLWYRPPDALLGATEYSSSELDIWAGCI
FIEMFQQOPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPWFPLPTPRSLHV
VWNLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV
RLKPEMCDLLASYQKGHPAQFSKCW

SEQ ID NO: 169_AA626859_H

NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIKICDFGFAQILIPGD
AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
TLGKLI PRHQSI FKSNGFFHGISIPEPEDMETLEEKFSVHPVALNFMKGCLKMNPDRL
TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQONQLLPLIPGSHISPTPDGRKQVLQK
FDHLPNI

SEQ ID NO: 170_AA061797_M

KIALREIRMLKLKHPNLVNLIEVFRKRKMHLVFEYCDHTLLNELERNPNGVSDGVIKSV
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMKICDFGFARILIPGDAYTDYVATRWY
RAPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI PRHQSI
IFRSNQFFRGISIPEPEDMETLEEKFSNVQPVALSFMKGCLKMNPDRLTCAQLLDSAYF
ESFQEDQMKRKARSEGRSRRRQONQLLPLIPGSHISPTPDGRKQVVQLKFDHLPNI

SEQ ID NO: 171_AA397553_H

MPNSERHGGKKDGSAGTLQPSGGGSSNSRERHRLVSKHKRHSKHSKMDGLVTPEA
ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSDRLHKHRRHQRHRSR

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FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRI SGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH
 KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSDDSSKQDDSPSGA
 SYGQDYDLSPSRSHTSNNYDSYKKSPGSTSRQSVSPPYKEPSAYQSSTRSPSPYRRQR
 SVSPYRRRRSSSYERSGSYSGRSPSPYGRRRSSSPFLSKRSLRSPLPSRKSMKSRSRSP
 AYSRHSSSHSKKKRSSSRSRHSSISPVRPLPLNSSLGAELSRKKKRAAAAAAAKMDGKES
 KGSPVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTTEVKNSSDTGK
 VKLDENSEKHLVKDLKAQGTDRDCKPIALKEEIVTPKETETSEKETPPPLPTIASPPPLP
 TTTTPPPQTPLPLPLPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSKTSASVSSQAN
 SQPPVQVSVKTQVSVTAAPHLKTSTLPLPLPLPLPGGDDMDSPKETLPSKPVKKEKEQ
 RTRHLLTDLPLPELPGGDLSPDSEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG
 KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPITAI REIKILRQ
 LIHRSVNMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDLMLGLESGLVHFSEDHIKFSM
 KQLMEGLEYCHKKNFLHRDIKCSNILLNNSGQIKLADFGRLARLYNSEESRPYTNKVITLW
 YRPPPELLLGEERYTPAIDVWSCGILGELFTKKPIFOANLELAQLELISRLCGSPCPAVW
 PDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLDLHMLTLDPSKRCTAEQTLQSDFL
 KDVELSKMAPDPLPHWQDCHELWSKKRRRQRQSGVVVEEPPPSKTSRKETTSGTSTEPVK
 NSSPAPPQPAPGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDL SIPQMAQLLNI
 HSNPEMQQLEALNQSISALTEATSQQODSETMAPEESLKEAPSAPVILPSAEQMTLEAS
 STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQGPRRTPTMPQEEAAACPPHIL
 PPEKRPPEPPGPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPEH
 QALRPMEYSTRPRPNRTYGNTDGPETGFSADTDERNSGPALTESLVQTLVKNRTFSGSL
 SHLGESSYQGTGSVQFPGDQDLRFARVPLALHPVVGQPFLLKAEGSSNSVVAETKLQNY
 GELGPGTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVY

SEQ ID NO: 172_AA789239_H

MEMYETLGKVGEGSYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE
 NLVNLIIEVFRQKKIHLVFEFIDHTVLDELQHYCHGLESKRLRKYLFOILRAIDYLSNN
 VIIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVLDKTSYG
 KYVPVDI WALGCMIIEMATGNPYLPSSSDLDLLHKIVLVXFMPELKAKLLQEAKVNSLI
 KPKESSKENELRKDERKTVYTNLLSSSVLGKEIEKEKKPKEIKVRVIVKVGGRGDI SEP
 KKKEYEGGLGQQDANENVHMPSPDTKLVTIEPPNPINPSTNCNGLKENPHCGGSVTMPPI
 NLTNSNLMAANLSSNLFHPSVRLTERAKKRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI
 FNERTGHSDQMANENKRKLNFSDRKEFHFPPELPTIQSKDTKGMEVKQIKMLKRESKK
 TESSKIPTLLNVDQNEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173_AA124976_M

LADIVHACLOIDPAERTSSTDLLRHDYFTRDGFIEKFIPELRAKLLQEAKVNSFIKPEN
 FKENEPVRDEKKS VFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIKAKGGKGDVPDQKKP
 EYEGDHRQQGTADDTQPSSLDKKPSVLELTNPLNPSENSDGVKEDPHAGGCMIMPPINLT
 SSNLLAANLSSNLSHPNSRLTERTKKRTSSQTIGQTLNSNRQEDTGPTQVQTEKGAFNE
 RTGQNDQISSGNKRKLNF PKCDRKEFHFPPELPTVQAKEMKGMVKQIKVLKRESKKTDS
 SKIPTLLSMDPNQEKQEGGDGDCEGNLKRNRFFFSR

SEQ ID NO: 174_AA575635_M CCRK_M

SASGQLKIADFGRLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVDLWAVGCIMG
 ELLNGSPLFPGENDIEQLCCVLRILGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVL P
 DASPQALDLLGQFLLYPPRQRIASQALLHQYFFTAPLPAHPSELPIQRPGGGPAPKAHP
 GPPHVHDFHVDRIEESLLNPELIRPFIPEG

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FIGURE 1N

SEQ ID NO: 175_AA631990_H

MITSISTEKSNGTHYPPMITTLQYYRGRGGKTAVVRHFS AEGPF AFAEMRHSKRTHCPDW
 DSRESWGHESYRGSHKRKRSHSSTQENRHCKPHHQFKESDCHYLEARSLNERDYDRRY
 VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSEIV
 DTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAAARSEIQVLEHLNSTDPNSVFR
 VQMLEWFDHGHVCI VFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHNNKL
 THTDLKPENILFVKSDYVVKYNSKMKRDERTLKNNTDIKVDFGSATYDDEHHSTLVSTRH
 YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVVFQTHDSKEHLAMMERILGPI PQHMIQ
 KTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQ
 RITLDEALQHPFFDLLKKK

SEQ ID NO: 176_AA557536_H

MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDL SRQERNWPSWA
 PEHSPSWPSSRLRLSPQEFGDHPNII SLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGG
 LQDVHVRISIFYQLLRATRFLHSGHVHRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG
 PEDQAVTEYVATRWYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT
 STLHQLELILETIPPPSEEXRPRQTL DALLPPDTSPEALDLLRLLVFAPDKRLSATQAL
 QHPYVQRFHCP SDEWAREADVRPRAHEGVQLSVPEYRSRVYQMI LECGGSSGTSREKGP
 GVSPSQAHHLKPRADPQLPSRTPVQGP RP RPQSSPGHDPAEHESPRAAKNVPRQNSAPLL
 QTALLNGERPPGAKEAPPLTSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV
 RVASVQVPPRLPPEARPGRRMFSTSALQGAQGGARALLGGYSQAYGTVCHSALGHLPLLE
 GHV

SEQ ID NO: 177_N28606_H, MOK_H

MKNYKAIGKIGEGTFSEVMKMQLRDGNYYACKQMQR FESIEQVNNLREIQALRRLNPH
 PNILMLHEVVFRKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH
 RNGIFHRDVKPENILIKQDV LKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFTY
 YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKILTKFKQSRAMNFD
 FPKGSGIPLLTNLS PQCLSLLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR
 KAGFPEHPVAPEPLSNSCQISKEGRKQKQSLKQEE DRPKRRGPAYVMELPKLKLSGVRL
 SSYSSTLQSVLGS GTNGRVPVLRPLKCI PASKKTD PQDLKPAPQOCRLPTIVRKGR

SEQ ID NO: 178_AB023153_H, ICK_H

MNRYTTIRQLGDGT YGSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKLNHA
 NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLFPESAIRNIMYQILQGLAFIHKLG
 FFHRDLKPENLLCMGP ELVKIADFLAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP
 IDVWAVGCIMAEVYTLRPLFP GASEIDTIFKICQVLGTPKKT DWPEGYQLSSAMNFRWPQ
 CVPNNLKTLPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS
 EKPQKGILERAGPPPYIKPVPPAQP PAKPHTRISSRQH QASQPPLHLTPYKAEVSRTDH
 PSHLQEDKPSPLLPFSLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKDSDDWAD
 LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVG TGNAPTQTSYQRRDTP
 LRSAAKQHYLKH SRYLPGISIRNGILSNPGKEFIPPNPWSSSGLSGKSSGTMSVISKVN
 VGSSSTSSSGLTGNVYPSFLKKEIGSAMQRVHLAPI DPSPGYSSLKAMRPHGRPF LDT
 QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179_AA839940_M

SSNNGGMSAEEEEIGPAEPMRGP SLATRDWRDET VGT TDLQQIDPGAVSPEPGKDHA AQ
 GPGRTEAGRVSSAAEAAI VVLDSSAAPPAPFEHRVVS IKDTLISAGYTVSQHEVLGGGRF
 GQVHRCTERSTGLALAAKI I KVNVDKREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT
 LIMEYVDGGELFDRITDEKYHLTELDVVL FTRQICEGVHYLHQHYILHLDLKPENILCVS

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FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL
SGLSPFLGETDAETMNFIVNCSWDFDADTFKGLSEEAKDFVSRLLVKEKSCRMSTQCLK
HEWLNHLPAKASGSNVRLRSQQLLQKYMAQSKWKKHFFHVAAVNRLRKFPCTCP

SEQ ID NO: 180_AA460132_H

MAAARATTPADGEEPAPEAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVLDLYVLEKAFLLSTHPNTETVFEAFKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 181_SGK034_H

QREKVNQGNMPLQSTFLAMDTTEEGVEVVWNLHFGDRKAFAAHEEKIQTTFEQLVLDH
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKTKKNHKAMNARAWKRWCTQILS
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSINALPDDLRSPIRAEREELR
NLHFFPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNQDTRVTEEAIRARHSLSDPNM
REFILCCLARDPARRPSAHSLLFHRVLFVHSLKLLAAHCFIQHQYLMPEENVVEEKTAM
DLHAVLAELPRRRPPLQWRYSEVSFMELEDFLEDVRNGIYPLMNFAATRPLGLPRVLAP
PPEEVQAKTPTPEPFDSETRKVIQMCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLL
PTDSAQDLASELVHYGFLHEDDRMKLAFLFLESTFLKYRGTOA

SEQ ID NO: 182_AA103218_M SGK034_M

HASAPYGEVNDGTGFVDIFSFGMCALEMAVLEIQANGDTRVTEEAIRARHSLSDPNMR
EFILSCLARDPARRPSAHNLLFHRVLFVHSLKLLAAHCFIQHQYLMPEENVVEEKTAM
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLLEDVRNGIYPLMNFAAARPLGLPRVLAP
PEEAQKAKTPTPEPFDSETRKVVQMCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLP
TDSAQDLAAELVHYGFLHEDDRTKLAFLFLETTFLKYRGTOA

SEQ ID NO: 183_NEK7_H, N34132_H

MSGGAEEKQSSTPGSLFLSPPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT
MDKDSRGAAATTTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAPVQSAPPEPH
REETVTATATSQVAQPPAAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPP
ARSGSGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRSFKTVYKGLD
TETTVAVWCELQDRKLTKEERQRFKEEAEMKGLQHPNIVRFYDSWESTVKGKKCIVLV
TELMTSGTLKTYLKRKFVKMIKVLRSWCRQILKGLQFLHTRTPLIIHRDLKCDNIFITGP
TGSVKIGDLGLATLKRAFAKSVIGTPEFMAPEMYEKEYDESVDVYAFGMCMLEMATSEY
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIEGCIQNKDERYSIKDLLNHAFFQ
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESLKKQVEQSSASQ
TGKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQQLQYQQPSISVLSDGTVDGQGG
SSVFTESRVSSQQTVSYGFPXHEQAHSTGTVPGHIPSTVQAQSQPHGVYPPSSVQQGIQQ
TAPPOQTVQYSLSQSTSSSEATTAQPVSQPAPQVLPQVSAGKQSTQGVSVQVAPAEVAV
AQPOATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRRHE
KTSRPKLRILNVSNKGDVVVECQLETHNRKMVTFKFDLDGDNPEEIIATIMVNDFILAIE
RESFVDQVREIEKADEMLSEDVSVEPEGDQGLSLOGKDDYGFSGSQKLEGEFKQPIPA
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN
LSHSASSLSLQAFSELRRQMTEGPNTAPPNFSHTGPTFPVVPFLSSIAGVPTTAAAT
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSVV
SSITIPAVVISITTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGPKPPA
VVSQQAAGSTTVGATLTSVSTTSFSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

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FIGURE 1P

HSSTTGLAFSLSAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL
 LPQVPSIPPLVQPVANVPAVQQTLIHSQPQAPALLPNQPHTHCPEVDSDTQPKAPGIDDIK
 TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP
 TNLPLGTVALPVTVPVTPGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTETLPAAGTL
 PSEQLPFPFPGPSLTQSQQPLEDLDAQLRRTLSPMITVTSVAVGPVSMAPTAITEAGTQP
 QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAAADGAQKEGKNKSEDAKSVHFESSTSESS
 VLSSSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTAN
 KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSD
 PEAFLSRDVEDDGGSGSPHSPHQLSSKSLPSQNLSQLSNSFNSSYMSSDNESDIEDDLK
 LELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVP PAVIIPPAAPLSGRRRRPTKSKGS
 KSSRSSSLGNKSPQLSGNLGQSAASVLHPQOTLHPPGNIPESGQNQLLQPLKPSPPSSDN
 LYSFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184_BCON3_H

MSEGESQTVLSSGSDPKVSSSSAPGLTSVSPVPTSTTSAASPEEEEESEDESEILEESP
 CGRWQKRREEVNQRNVPGIDSAYLAMDTTEGVEVWNEVQFSEKKNYKLOEEKVRAVFDN
 LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKTCKNHNKTMNEKAWKRW
 CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHVKTCTREEQKNL
 HFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNGGESSYVPQEAISSAIQLLEDPLQ
 REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAAHCIVGHQHMI PENALEEITKNM
 DTSAVLAEIPAGPGREPVTLYSQSPALEDKFLVDVRNGIYPLTAFGLPRPQQPQQEEV
 TSPVPPSVKTPTEPAEVEVTRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRLHSCDL
 MPNENIPELAAELVQLGFISEADQSRLTSLEETLNKFN FARNSTLN SAAVTVSS

SEQ ID NO: 185_AA711829_M

LKQFLKKTCKNHNKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK
 IGSVAPDTINNHVKTCTREEQKNLHFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNG
 GESSYVPQEAISSAIQLLEDLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAA
 AHCIVGHQHMI PENALEEITKNMDTSAVLAEIPAGPGREPVTLYSQSPALEDKFLVDV
 RNGIYPLTAFGLPRPQQPQQEEVTSPVPPSVKTPTEPAEVEVTRKVVLMQCNIESVEEG
 VKHHLTLLLKLEDKLNRLHSCDLMPNESIPDLAAELVQLGFISEADQSRLTSLEETLNK
 FNFTRNSTLN TATVTVSS

SEQ ID NO: 186_AA099102_H

MSSCVSSQPSSNRAAPQDELGGRGSSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP
 GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR
 CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVK
 LAYNENDNTYYAMKVLSSKKLIRQAAPRRPPPRGTRPAPGGCIQPRGPIEQVYQEIAIL
 KKLDHPNVVKLVEVLDDPNEDHLYMVFEVLNQGVPMEVPTLKLPLEDQARFYFDLIKGI
 EYLHYQKIIHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGT PAFMAPESLS
 ETRKIFSGKAKDVWAMGVTL YCFVFGQCPFMDERIMCLHSKIKSQALEFPDQPDIAEDLK
 DLITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENS VKHIPS
 LATVILVKTMIKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP
 PGRHPAPRGGGGSALVRGSPCVESCWAPAGSPARMHPLRPEEAMEPE

SEQ ID NO: 187_5R69_17_2_H

MQEIPQEQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR
 QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGT LRELLDREKDLTLG

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FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVLTQGYQVKLAGFELRKTQTSM SLGTT
REKTRDRVKSTAYLSPQELEDVFYQYDVKSEIYSFGIVLWEIATGDI PFQGECECDWLSQW
L

SEQ ID NO: 188_H85811_H

MAPVYEGMASHVQVFS PHTLQSSAFCSVKLKI EPSSNWDMTGYGSHSKVYSQS KNIPLS
QPATTTVSTSLPVPNPSPYEQTIVFP GSTGHIVVTSASSTSVTGQVLGGPHNLMRRSTV
SLLDITYQKCGLKRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS
EGDYQLVQHEVLC SMTNTYEVLEFLGRGTFGQVVKCWKRGTNEIVA I KILKNHPSYARQG
QIEVSILARLSTESADDYNFVRAYECFQHKNHTCLVFEMLEQNL YDFLKQNKFSPLPLKY
IRPVLQQVATALMKLSLGLIHADLKPENIMLVDP SRQPYRVKVIDFGSASHVSKAVCST
YLQSRYYRAPEI I LGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP
AEYLLSAGTKTTRFFNRD TDSPLYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN
MTTDLEGS DMLVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSTH
VKSCFQNM EICKRRVNM YDTVNQSKTPFITHVAPSTSTNL TMTFNNQLTTVHNQPSAASM
AAVAQRSMPLQTGTAQICARPD PFQQA LVCPPGFQGLQASPSKHAGYSVRMENAVPIVT
QAPGAQPLQIQPGLLAQQA WPSGTQQILLPPAWQQLTG VATHTSVQHATVIPETMAGTQQ
LADWRNTHAHGSHYNPIMQOPALLTG HVTLPAAQPLNVGVAHV MRQQPTSTTSSRKSQKH
QSSVRNVSTCEVSSSQAISSPQRSKRVKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT
RERQRTIVIPDTPSP TVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDS PYS
DSSSNTSPYSVQQRAGHNNANAFDTKGSLE NHCTGNPRTI IVPPLKTQASEVLVECD SLV
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITYROQRPGPHFQQQQPLNLSQAQQHI
TTDRGTGSHRRQAYITPTMAQAPYSFPHNSPSHGT VHPHLAAAAAAHLPTQPHLYTYTA
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQVPVSMGPRVLPSP TIHPSQYPAQF
AHQTYISASPASTVYTGYP LSPAKVNQYPYI

SEQ ID NO: 189_DYRK3_H

MMIDETKCPPCSNVLCNPSEPPPPRRRLNMTAEQFTGDHTQHFLDGGEMKVEQLFQEFGNR
KSNTIQSDGISDSEKCSPTVSQ GKSSDCLNTVKSNSSSKAPKVVPLTPEQALKQYKHHLT
AYEKLEI INYPEIYFVGPNAKKRHGVIGGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII
GKGSFGQVARVYDHKL RQYVALKMVRNEKRFH RQAABEIRILEHLKKQDKTGSMNVIHML
ESFTFRNHVCM AFELLSIDLYELIKKNKFQGSFVQLVRKFAQSILQSLDALHKNKI IHCD
LKPENILLKHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEI ILGSRYSTPIDIWSF
RCILAELLTGQPLFPGEDEGDQLACMMELLMPPPKLLEQSKRAKYFINSKGI PRYCSVT
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKG CDDYLFIEFLKRCLHWDPSARLTPAQ
ALRHPWISKSVPRPLTTIDKVS GKRNVNPASAFQGLGSKLPPVVG IANKLKANLMSETNG
SIPLC SVLPKLIS

SEQ ID NO: 190_AA589241_M DYRK3_M

TRPELLGMPPQKLLEQSKRAKYFINSKGLPRYCSVSTQTDGRVLLGGRSRRGKKRGPPG
SKDWATA LKGC GDYLFIEFLKRCLQWDPSARLTPAQALRHPWISKSTPKPLTMDKVPGKR
VVNPTNAFQGLGSKLPPVVG IASKLKANLMSETSGSIPLC SVLPKLIS

SEQ ID NO: 191_5R72_16_2_H

MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDAGPVKEPPEINLVLY
PQGLTGEEVYVKVDLRVKCPPTYPDVVP EIELKNAKGLSNESVNLLKSRLEELAKKHCGE
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQQRLLLEAKRKEEQEQREILHEIQ
RRKEEIKEEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHGGS P D FVNGKXHR
ANSSGRSRRERQYSVCNSEDSPGSCEILYFNMGSPDQLMVHKGKCI GSDEQLGKLVYNAL
ETATGGFVLLYEWVLQWQKKMGF L TSQEKEKIDKCKKQIQGTETEFNSLVKLSHPNVVR

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FIGURE 1R

YLAMNLKEQDDSIIVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLSNS
VVHKVLSASNVLVDAEGTVKI TDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD
VWRLGLLLLLSLSQGECEYPTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFIN
PQPKMPLVEQSPEDSGGQDYVETVIPSNRLPSAAFFSETQRFQFSRYFIEFEELQLLGKA
FGAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVRYYNWIERHE
RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVIEWSTSGERSAS
ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSESDI IFDNEDENSKSNQDEDCNEK
NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
EKGMIHRLDKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTDGLIKSDPSGHLTG
MVGTAIYVSPEVQGSTKSAYNQKVDLFSLGI IFFEMSYHPMTASERIFVLNQLRDPTSP
KFPEDFDDGEHAKQKSVISWLLNHDPKRPTATELLKSELLPPPQMEESSELHEVLHHTLT
NVDGKAYRTMMAQIFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIRIFKRHGA
VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE
RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEI IYTIYEI IQEFPALQERNYSIYL
NHTMLLKAILLHCGIPEDKLSQVYI ILYDAVTEKLTRREVEAKFCNLSSNSLCLRYKF
IEQKGDLDLMPNTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK
VQQHNGI IFQFVAFI KRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIADK
ISAAVLNMEESVTISSCDLLVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
EYCRHHEITYVALVSDKEGSHVKVSFEKERQTEKRVLETELVDHVLQKLRTKVTDERNG
REASDNLAVQNLKGSFSNASGLFEIHGATVVP IVSVLAPEKLSASTRRRYETQVQTRLQT
SLANLHQSSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
DEIYNIKVEKKVSVLFLYSYRDDYRILF

SEQ ID NO: 192_R43524_H, HRI_H

MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP
FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFLLCQTFIKMGLLSSFTCSDEFSSRLHH
NRAITHLMRSKERVVRQDPCEDISRIQKIRSREVALEAQT SRYLNEFEELVILGKGGYGR
VYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREVKVLAGLQHPNIVGYHTAWIEHVHI
QPRADRAAIELPSLEVLSDQEEDREQCGVKNDSESSSSIIFAEPTPEKEKRFGESDTENQ
NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQPLRRNSHLEESFTSTEE
SSEENVNFLGQTEAQYHMLHMQMLCELSLWDWIVERNKRGREYVDESACPYVMANVAT
KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDPQVKIGDFGLACTDILQKNTDWTNRN
GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSGLGVVLELFPQFPGTEMERAEVLTGL
RTGQLPESLRKRCVPQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLMKII EQ
EKEIAELKKQLNLLSQDKGVRDDGDKGGVG

SEQ ID NO: 193_17000057519457_H

MAAARATTPADGEEPAPAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEEIEGVS
TVRDYIQSTMETEKTPOGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFI SALPEDKGVLDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 194_AA013524_M

LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPLEEARLGRRRTVQEARALLRCRRAGIA
APVVFVDYASNCLYMEEIEDSVTVRDYIQSTMETEKDPQCLLDLARRMGQVLAMHDQD
LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFSVGLPEDKGVLDLYVLEKAFLSTHPHTETA
FEAFLKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

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FIGURE 1S

SEQ ID NO: 195_17000139801197_H, IRAKM_H
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK
YVDQKGSGTRELLWSWAQKNKTIGDLLQVLQEMGHRRAIHLITNYGAVLSPSEKSYQEGG
FPNILFKETANVTVDNVLIPHEHNEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY
RVEIQNLTYAVKLFKQEKMMQCKKHWRFLSELEVLLLFHHPNILELAAYFTETEFKCLI
YPYMRNGTLFDR LQCVGDTAPLPWHIRIGILIGISKAIHYLHNVPQCSVICGSISSANIL
LDDQFQPKLTDFAMAHFRSHLEHQSC TINMTSSSSKHLWYMPEEYIRQGKLSIKTDVYSF
GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRG LDSCLSFLDKKVP PCPRNFS AKLFC
LAGRCAATRAKL RPSMDEV LNTLESTQASLYFAEDPPTS LKSFRCPSPLFLENVPSIPVE
DDESQNNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSCE
ESWFPKYIVPSQDLRPYKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196_AA840598_M IRAKM_M
MWKRF LSELEVLLLFRRHPHILELAAYFTETEFKLC LVYPYMSNGTLFDR LQCTNGTTPLSW
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ
SSTINMTGGGRKHLWYMPEEYIRQGR LSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR
DLLMELMEKRG LDSCLSFLDRKIPPCPRNFS AKLFLAGRCVATKAKLRPTMDEV LSSLE
STQPSLYFAEDPPTS LKSFRCPSPLFLDNVPSIPVEDDENQNNH SVPPKEVLGTDRVTQK
TPFECSQSEVTFGLDRNRGNRGSEADCNVPSSSHEECWSPELVAPSQDLSPTVISLGSS
WEVPGHSYGSKPMKRCSSGLFCSEHEQSKKQ

SEQ ID NO: 197_AA088547_H
MASAVRGSRPWPRLGLQLQFAALLGLT LSPQVHTLRPENLLL VSTLDGSLHALSKQTGDL
KWTLRDDPVIEGPMYVTEMAFLSDPADGSLYILGTQKQOGLMKLPFTIPELVHASPCRSS
DGVFYTG RKQDAWFVVD PESGETQMTLTTEGPSTPRLYIGRTQYTVTMHDPRAPALRWNT
TYRRYSAPPMDGSPGKYM SHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHDGL
RQLPHLT LARDTLHFLALRWGHIRLPASGPRDTATL FSTLDTQLLMTLYVGKDETGFYVS
KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYP SG SVALPSQWLLI
GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK
TPDSYLGLGPQDLLAASLTAVLLGGWILFVMRQVVEKQQETPLAPADFAHISQDAQSLHS
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFFVFRGQFEGRA
VAVKRLRECFGLVRREVQLLQESDRHPNVLRYFCTERGPOFH YIALELCRASLQEYVEN
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGN ILITGPDSQGLGRVVLSDFGLC
KKLPAGRCFSLSHSGIPGTEGWMAPELLQLLPDSPTS AVDIF SAGCVFYVLSGGSHPF
GDSLYRQANILT GAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSR
AKQLQFFQDVSDWLEKESEQEPLVRAL EAGGCAVVRDNWHEHISMPLOTDLRKFRSYKGT
SVRDLLRAVRNKKHHYREL PVEVRQALGQVPDGFVQYFTNRFPRLLLHTHRMRSCASES
LFLPYYPDPDSEARRPCPGATGR

SEQ ID NO: 198_HGP_6644466
MEGISNFKTPSKLSEKKKS VLCSTPTINIPASPFMQKLGF GTGVNVYLMKRSPRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE
KSLNDLIEERYKASQDPFPAAIILKVALNMARG LKYLHQEKLLHGD IKSSNVV IKGDFE
TIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEAVEENGVI TDKADIFAFGLTLWEM
MTLSIPHINLSNDDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDES YQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199_AA449542_M
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKNLHNPNIIGYRAFTEASDGSL
CLAMEYGGEKSLNDLIEERNKDSGSPFPAAVILRVALHMARG LKYLHQEKLLHGD IKSS

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FIGURE 1T

NVVIKGFETIKICDVGVSPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV
AFGLTLWEMMTLCIPHVNLPDDDDVEDATFDESDFDDEAYYAALGTRPSINMELDDSYQK
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200_5R57_10_2_M TESK2_M
LLSDSLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201_AA232253_H
MSSLGASFVQIKFDDLQFFENC GGGSFGSVYRAKWISQDKEVAVKLLKIEKEAELSVL
SHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWATDVAKGMHY
LHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFFPWWAPEVIQS
LPVSETCDTYSYGVVLWEMLTREVFPKGLEGLQVAWLVEKNERLTI PSSCPRSFAELLH
QCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRCIEATLERLKKLERD
LSFKEQELKERERRLKMWEQKLTEQSNTPLLPSFEIGAWTEDDVYCWWQQLVRKGDSSAE
MSVYASLFKENNITGKRLLLLLEEDLKDMGIVSKGHI IHFKSAIEKLTHDYINLFHFPPL
IKDSGGEPEENEKIVNLELVFGFHLKPGTGPQDCKWKMYMEMDGEIAITYIKDVTFTNT
NLPDAEILKMTKPPFVMEKWIIVGIAKSQTVECTVTYESDVTRTPKSTKHVHLIQWSRTKPQ
DEVKAVQLAIQTLFTNSDGNPGSRSDSSADCQWLDTLRMRQIASNTSLQRSQSNPILGSP
FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSSPTQYGLTKNFSSLHLNSRDSGFS
SGNTDTSSERGRYSDRSRNKYGRGSI SLNSSPRGRYSQHSQSTPSRGRYPGKPYRVSQS
ALNPHQSPDFKRSRDLHQPNITPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202_AI375137_H
MGNYKSRTQTCTDEWKKVSESYVITIERLEDDLQIKEKELTELNRNIFGSDEAFSKVNL
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL
LHSGADIQQVGYGGLTALHIATIAHLEAADVLLQHGAVNIQDAVFFTPLHIAAYYGHE
QVTRLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVPPLH
FCSRFGHHDIVKYLLQSDLEVQPHVNIYGDTPHLACYNGKFEVAKETIIQISGTESLTK
ENIFSETAFHSACTYGKSIDLKFLDQNVININHQRDGHGTGLHSACYHGHIRLVQFLL
DNGADMNLVACDPSRSSGEKDEQTCMLWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG
GDGSYVSVPSPLGKIKSMTKEKADILLRAGLPSHFHLQLSEIEFHEIIGSGSFGKVYKG
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIOFVGACLNDSQFAIVTQ
YISGGSFLSLLHEQKRILDLQSKLIIADVAKGMEYLHNLTPQPIIHRDLNSHNILLYEDG
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT
GEIPFAHLKPAAAAAD MAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA
LSQSAGQYSSQGLSLEEMKRSLOQYTPIDKYGYVSDPMSSMHFHSRNSSSSFEDSS

SEQ ID NO: 203_H97685_H
MESERSPLYROLIDLGYLSSSHWNC GAPGQDTKAQSMLEQSEKLRHLSTFSSHQVLQTRL
VDAKALNLVHCHCLDIFINQAFDMQDRLQITPKRLEYTRKKENELYESLMNIANKQEE
MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEPVGTREIKCCIRQIQELIISRNLQA
VANKLISSVDYLRESFVGTLECLQSLEKSQDVSVHITSNYLKQILNAAHYVEVTFHSGS
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTLNS
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHPRLARLSLESRLQDVLLHRKPKLG
QELGRGQYGVVYLCDNWGGHFP CALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
SVIDYNYGGGSSIAVLLIMERLHRDLTYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH
RDIKLNVLDDKQNRAKITDLGFCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

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FIGURE 1U

ILFWYICSGSVKLEPAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK
RPLLGI VQ PMLQ GIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204_W20810_M

DVNLKASKASDVYSFGILVWAVLAGREAELVDKTS LI RETVCDRQSRPPLTELPPGSPET
PGLEKLKELMIHCWGSQSENRP SFQDCEPKTNEVYNLVKDKVDAVSEVKHYLSQHRSSG
RNLSAREPSQRGTEMDCPRETMVSKMLDRLHLEEPSGVPVGKCPERQAQDTSVGPATPAR
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHQPNQGDGRHGTWPYPWTPPNPMTGP
PALVFNNCSEVQIGNYNLSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205_AA744236_H

MGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYKRENE DKVNKAAKHLKTL
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSAEVCAGIYDILLALIFLHDRGHL
THNNVCLSSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPEFTT
LPECHGHARDAFSFGTLVESLLTILNEQVSADVLSSFQOTLHSTLLNPIPKCRPALCTLL
SHDFFRNDLFLEVNF LKSLTLKSEEEKTEFFKFLDRVSC LSEELIASRLVPLLLNQLVF
AEPVAVKSFLPYLLGPKDHAQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLISH
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSDVKNTSEDS ENFPSSSKKSEEPDWSE
PEEPENQTVNIQIWPREPCDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG
LGEEFTIQVKKKPKVDPEMDWFADMIPEIKPSAAFLILPELRTEMVPKKDDVSPVMQFSS
KFAAAEITEGEAEGWEEEGELNWNEDNNW

SEQ ID NO: 206_AI052250_H

MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE
VAVFVFDKKLIDKYQKFEKDQIIDSLKRGVQQLTRLRHPRLLT VQHPLEESRDCLAFCTE
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT
PENIILNKSGAWKIMGFD FCVSS TNPSEQEPKFCKEWDPNLPSLCLPNPEYLAPEYILS
VSCETASDMSYSLGTVMYAVFNKGKPIFEVNKQDIYKSFSRQLDQLSRLGSSSLTNIPEEV
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTL FQRDNLQKSQFFKGLPKVL
PKLPKRIVIVQRILPCLTSEFVNPDMPFVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ
EPIQIILLIFLQKMDLLT KTPPDEIKNSVLP MVYRALEAPSIQIQELCLNIPTFANLID
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207_AA278842_H

MWFFARDPVRDFFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEEQTQV
AKAAFKRFTLRHPNILAYIDGLETEKCLHVVT EAVTPLGIYLKARVEAGGLKELEISWG
LHQIVKALSFLVNDCSLIHNNVCM AAVFVDRAGEWKLGG LDYMYSAQNGGGPPRKGIPE
LEQYDPP ELADSSGRVVREKWSADMWRLGCLIWEVFNGPLPRAAALRNPGKIPKTLVPHY
CELVGANPKVRPNPARFLQNCRAPGGFMSNR FVETNLFLEEIQIKEPAEKQKFFQELSKS
LDAFPEDFCRHKVLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS
TDRAMRIRLLQOMEQFIQYLDEPTVNTQIFPHVVHGF LDTNPAIREQTVKSMLLLAPKLN
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDFF
APSRVAGVLGFAATHNLYSMNDCAQKILPVL CGLTVDPEKSVRDQAFKAIRSFLSKLESV
SEDPTQLEEVEKDVHAASSPGMGGAASWAGWAVTGVS SLTSKLIRSHPTTAPTETNIPQ
RPTPEGVPAPAPTVPATPTTSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVL
AQQDDWSTGGQVSRASQVSNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEP PPDGTR
LASEYNWGGPESSDKGDPFATLSARPSTQPRPDSWGEDNWEGLETD SRQVKAELARKKRE
ERRREMEAKRAERKVAKGPMKLGARKLD

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FIGURE 1V

SEQ ID NO: 208_AA599286_H

MAFMEKPPAGKVLDDTVPLTAAIEASQSLQSHTEYIIIRVQGGISVENSWQIVRRYSDFD
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD
PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSW
ADLGPDKYLSDKDFQCLIKLLPSCLPYIYRVTFATANESSALLIRMFNEKGTLDLIYK
AKPKDPFLKKYCNPKKIQGLELQIKTYGRQILEVLKFLHDKGFPYGHLSHNSVMDLGD
CRLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP
PAPSMVAVVLESTLSCEACKNGMPTISRLLQMPFLSDVLLTTSEKPFKIPTKLKEALR
IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEERKKRKILARKKSKRSALENSEEHS
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEAPQLS
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRRAEASCLHLEGKVLFYSSPLPPN
YPLPGKVIAEPVQPQTVLFCRCSCCKQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209_AA425725_H

MSASTGGGGDSGGSGSSSSSQASCGPESGSELALATPVPQMLQGLLGSDDEEQEDPKD
YCKGGYHPVKIGDVFNTRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVKSAHYTETA
VDEIKLLKCVRSDSPDPKRETIVQLIDDFRISGVNGVHVCMLVLEVLGHQLLKWIISNY
QGLPVPCKSIVRQVLHGLDYLHTKCKIIHTDIKPENILLCVGDAYIRRLAAEATEWQQA
GAPPPSRISIVSTAPQEVLTGKLSKNKRKMRKRKQKRLLEERLRLDLQRLAMEAATQA
EDSGLRLDGGSGSTSSSGFSGLFSPASCSILSGSSNQRETGGLSPSTPFGASNLLVNP
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGPADIWSTACMAF
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDIPPAFALSGRYSREFFNRRGELRHIHN
LKHGWGLYEVLMKEYEWPLEQATQFSALLPMMEYIPEKRASAADCLQHPWLNP

SEQ ID NO: 210_SGK022_H

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ
IVRTL DHKNIIQVYEMLESADGKICLVMELEAGGDVDFCVLNGGGLPESRAKALFRQMV
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFAKVLPKSHRELSQTFCCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLSISADCQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 211_AA060026_M SGK022_M

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ
IVRTL DHKNIIQVYEMLESADGKIYLVMELEAGGDVDFCVLNGGGLPESRAKALFRQMV
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFAKVLPKSRRELSQTFCCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLGISTECQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 212_AA399669_H

MGKGDVLEAAPTTTAYHSLMDEYGYEVGKAIGHGSYGSVYEAFTYTKQKVMVAVKIISSKK
ASDDYLNKFLPREIQQVMKVL RHKYLINFYRAIESTSRVYIIILELAQGGDVLEWIQRYGA
CSEPLAGKWFSQLTLGIAYLHKSIVHRDLKLENLLLDKWENVKISDFGFAKMVPSNQPV
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLPF
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213_AA758539_H

MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE
MDILATVNHGSIKTYEIFETSDGRIYIIMELGVQGDLLFEIKCQGALHEDVARKMFRQL
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

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FIGURE 1W

YAAPEVLQSIPIYQPKVYDIWSLGVILYIMVCGSMFYDDSDIRKMLRIQKEHRVDFPRSKN
LTCECKDLIYRMLQPDVSQRLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHI SGAEVGKAST

SEQ ID NO: 214_AA883975_H
MSGDKLLSELGYKLGRITIGESYSKVKVATSKKYKGTVAIKVVDRRRAPDFVNKFLPRE
LSILRGVRPHIVHVFIEVCNGKLYIVMEAAATDLLQAVQRNGRIPGVQARDLFAQIA
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRAHGYPDLSTTYCGSAAYASP
EVLLGIPYDPKKYDVWSMGVVLVYVMVTGCMFDDSDIAGLPRRQKRGVLYPEGLELSERC
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215_AA905446_H
VGRQETGVRRWAF LICQIPSP L TSSEFIQRFLPRELQIVRTLDHKNI IQVYEMLESADG
KICLVMELAEAGDVDFDCVLNGGGLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALL
QGFNLKLTDFGFAKVLPKSHRELSQTF CGSTAYAAPEVLQGI PKMLWQQQKGVSFPTH
SISADCQDLLKRLLEPDMILRPSIEEVS WHPWLAST

SEQ ID NO: 216_H29974_H
YSLLAIEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAE EPCYLW FVMEFCEGG
DLNQYVLSRRPD PATNKS FMLQLTSAIAFLHKNHIVHRDLKPDN ILITERSGTPILKVAD
FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYMAPEVWEGHYTAKADI FALG
IIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG
IKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 217_AA498104_M H29974_M
PLLLPPPPAAMETGKENGARRGTS PERKRRSPVQRVLCEKLRPAAQAMDPAGAEVPGEA
FLARRRPDGGGDV PARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE
LALAEFWALTSLKRRHQNIVQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL
GYAE EPCYLW FVMEYCEGGDLNQYVLSRRPD PATNKS FMLQLTSAIAFLHKNHIVHRDLK
PDN ILITERSGTPILKVAD FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYM
APEVWEGHYTAKADI FALGIIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLE
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 218_AA215311_H
MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI
KSQHPNVHLEECILQKDG MVQKMSHGSSNSSLYLQLVETSLKGEIAFDPRSAYYLW FVMD
FCDGGMNEYLLSRKPNRKTNTSFMLQLSSALAF LHKNI IHRDLKPDN ILISQTRLDTS
DLEPTLKVAD FGLSKVCSASQNP EEPVSVNKCFLSTACGTD FYMAPEVWEGHYTAKADI
FALGIIIWAMLERITFIDTETKKELLGSYVKQGT EIVPVGEALLENPKMELLI PVKKKSM
NGRMKQLIKEMLAANPQDRPD AFELELRVLQIAFKDSSWET

SEQ ID NO: 219_AA018361_H
MRAAFPAGGAGGSVEPPSARPAQ PAGTAARSEEAPARAQAAGMAGPGWGPPRLDGFILT
ERLGS GTYATVYKAYAKKDTREVVAIKCVAKKSLNKASVENLLTEIEILKGIRHPHIVQL
KDFQWSDNIYLIMEFCAGGDL SRFIHTRRILPEKVARVFMQQLASALQFLHERNISHLD
LKPQNILLSSLEKPHLKLADFGFAQH MSPWDEKHVLRGSPLYMAPEMVCORQYDARVDLW
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDL LQRLLEDP SR
RISFQDFFAHPWVDLEHMPSGESLGRATALV VQAVKKDQEGDSAAALS LYCKALDFVPA

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FIGURE 1X

LHYEVDARKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARKPRLL
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSRAGGGSCFTLRFRTSWPELN
T

SEQ ID NO: 220_AA311714_H
MENFILIYEEIGRSGKTVVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIVT
FHEWYETSNHLWLVLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL
KFSNFCCLAKVEGENLEEFFALVAAEEGGDNGENVLKKSMKSRVKGSPVYTAPVVRGAD
FSISSDLWSLGLLYEMFSGKPPFFSESVSELTEKILCEDPLPPIPKDSSRPKASSDFIN
LLDGLLQDRDPQKRLTWTRLLQHSFWKKAFAAGADQESSVEDLSLSRNTMECSGPQDSKELL
QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPPTPTSTAVEV
SPGEDMTHCSPOKTSPLTKITSGHLSQQDLESQMRELIYTDSDLVVTPIIDNPKIMKQPP
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV
AGHQEVATRLHSPFLQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS
SIGIGILNCLVQHSTFPVPRQCLVYV

SEQ ID NO: 221_SGK384_H
SLAHVLRARQILTEPEVRDYLRGLVSGRLRYLHQRCILHR

SEQ ID NO: 222_AA210451_M SGK384_M
MGQQHGTNRGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPGRSTADSRRCPPGYFR
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH
GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNLKYQDVNTWQHRLQL
AMEYVSIINYLHHSPLGTRVMCDSDNLPKTLQYLLTSNFSIVANDLDALPLVDHDSGLV
IKCGHRELHGDFVAPEQLWPYGEDTPFQDDLMPSYNEKVDIWKIPDVSSFLGHVEGSDM
VRFHLDIHKACKSQIPAERPTAQNVLDAYQRVFHSRLRDTVMSQTKEML

SEQ ID NO: 223_SGK071_2_H
EVVAVQMMVECMDDHYASQALEELMPLLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALAYLHHLDIHRNLKPSNIIILISSDH
CKLQDLSSNVLMTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC
SFMGDTEAMHLRKSRLRQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD
VVHITFLRGSFKSSCVSLTLHRQMPASITDMLLEGNVASILGDAGDTKGERALKLLSMA
LASVCLVPEGSFLMPLALLHMDQWLSQDQDRVPGKRDFASLGKLGKLLGPPIKGLPWPP
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH
PEEEPLLVMVYSLLAITTTQESSESLSEELQNAAGLLEHILEHLNSSLERSDVCASGLGLLW
ALLLDDPILALQRPKRPNHGKPGKPNPASTQSIIVNKAPLEKVPDLISQVLATYPA
DGEMAEASCGVFWLLSLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKV
SELAAFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGMLLVHLASVYEEILPELVSSSM
KALLQEIKERFTSSSLVSDSSAFSKPGLPPGGSPQLGCTTSGGLE

SEQ ID NO: 224_AA118352_M SGK071_M
EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL
KPILKTMEEKQIPGTDVYLLLPFMLHINPSDRLAIKDVMQVTFMSNSFKSSSVNALNMQR
QKVPIFITDVLLGNMANILGSWLCASFVNDNRHCDSGIGSQRLGFDQSVSWTEHPLKD
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTLEEEVISIIKQHGRILDILLSTCSLL
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGQISEEL
EEEGFLQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVLVLLRSIQLCPGRVLLVNNAFRGLASLAK

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FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLOEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225_018653.9_H

GRGRGAGHARGLRGPAGRRAEPPRSLSRPGPGPSRAGPAGRGEESDAAPAGGSGRGFL
RLLPAGLRPQALRSGSEPPRPGQSPEPSAPGAGRRGGRGELARQIRARYEEVQRYSRG
GPGPGAGRPERRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA
ALRNVSGAQYMGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEIDPTLTTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI
LEFPARNFTLPCSAQGWCEGMNEKRNLNAYRFFFTYLLPHSAPPSLRPLLDSIVNATGE
LAWGVDETLAQLEKVLHLRSGQYLQNSTASSSTEYQCI PDSTI PQEDYRCWPSYHHGSC
LLSVFNLAEAVDVCESHAQCRAFVVTNQTTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226_AA396601_M

TRPGCAALRNVSGAQYVGSYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGARRG
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEIDPTLTTITELGAPVEMIQLLQTS
SWEDRFRICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLNAYRFFFTYLLPHSAPPSLRPLLDSI
VNATGELAWGVDETLAQLETLAHLFRSGQYLQNSTSSRAEYQRI PDSAITQEDYRCWPSY
HHGGCLLSVFNLAEAIDVCESHAQCRAFVVTNQTTWTGRKL VFFKTGWNQVVPDAGKTTY
VKAPG

SEQ ID NO: 227_VRK3_H

MISFCPCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPVHVSFQGSKRGLNSSFETSP
KKVKSSTVTSPRLSLFSDGDSSEEDTLSSSERSKSGSGSRPPTPKSSPQKTRKSPQVTR
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLSFQTRDNQGIL
YEAAPTSTLTCDSGPQKQKFSCLKDAKDGRLFNEQNFFQRAAKPLQVNWKKLYSTPLLA
IPTCMGFGVHQDKYRFLVLP SLGRSLQSALDVSPKHVLSERSVLQVACRLLDALFLHEN
EYVHGNTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFISMD
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP CGH
WIRPSETLQKYLKVVMALTYEEKPPYAMLRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228_S71575_M VRK3_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSALDDNPKHVVSERCVLQVACRLLDALFLHEN
EYVHGNTAENVFVNPEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFISMD
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTTEKITRQKQKYLDSPERLVGLCGR
WNKASETLREYLKVVMALNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMPV

SEQ ID NO: 229_AA45427_H

MGHALCVCSRGTVIDNKRFLFIQKLGEFFSYVDLVEGLHDGHFYALKRILCHEQQDRE
EAQREADMHRFLFNHPNILRLVAYCLRERGAKHEAWLLL PFFKRGTWNEIERLKDKNFL
TEDQILWLLL GICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLM DLGSMNQACIHVEGS
RQALTLDWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGCVL YAMMFEGGPYDMVFQ
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQPHIPLLSQLEALQPPAPGQ
HTTQI

SEQ ID NO: 230_H05721_H

MAVRQALGRGLQLGRALLRFTGKPGRAYGLRPGPAAGCVRGERPGWAAGPGAEP RRVG
LGLPNRLRFFRQSVAGLAARLQRQFVVRWGCAGPCGRAVFLAFGLGLGLIEEKQAESRR

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FIGURE 1Z

AVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRL E EYLIGSIGKGCSAAVYEATMPTLPQ
 NLEVTKSTGLLPGRGPGTSAPGEGQERAPGAPAFPLAIKMMWNISAGSSSEAILNTMSQE
 LVPASRVALAGEYGAVTYRKS KRGPQLAPHPNIIRVLRAFTSSVPLLPGALVDYDPDVL
 SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTSPRLAAMMLLQLLEGVDHLVQQGIAH
 RDLKSDNILVELDPDGCPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST
 ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGYQGAHLESRSYQEAQLPALPESVPP
 DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMGVWLLQOSAATLL
 ANRLTEKCCVETKMMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231_AI086865_H
 MEKYERIRVVGRAFGIVHLCLRKADQKLVIKQIPVEQMTKEERQAAQNECQVLKLLNH
 PNVEIYYENFLEDKALMIAMEYAPGGTLAEFIQKRCNSLLEETILHFFVQILLALHHVH
 THLILHRDLKTQNILDKHRMVVKIGDFGISKILSSKSTPCYISPCLCEGKPYNQKSDIW
 ALGCVLYELASLKRAFEAANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP
 PLSHIMAQPLCIRALLNLHTDGREVRGPQOQHQDHCPLQGIIMTFGSGSNGCLGHGS
 LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPILLSIDLGTAHSAAVTGEEDL
 GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPKCCWRHKQCTGHIIPFASDCV
 RSHSLHLSVNHNCNSRLKDSSSEDSSSSRGAGPTCSHVIESPCFELTPEEHVERFRYGW
 CKSYRPVSVAVIHHPLYHECGADDLNXXKRKRKRKRKRKPPIPTQVGPATASPDLTSMAT
 GTPDSTAPITIWRSPTGKGQGSKVIKKVKKKKEKEKDKEEMDEKAKLKKKAKKGQLTK
 KKSPVKLESPDPVSRSLARQLARMSSESPESREELESEDSYNGRGQELSSSEDIVESS
 SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232_AA836348_H
 MSVLGEYERHCDINSDFGSESGGCGDSSPGPSASQGPRAGGAAEQEELHYIPIRVLGR
 GAFGEATLYRRTEDDSLVWVKEVDLTRLSEKERRDALNEIVILALLQHDNIIAYYNHMD
 NTTLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVSCIHKAGILHRDIKTL
 NIFLTKANLIKLDYGLAKKLNSEYSMAETLVGTPYYMSPELCQGVKNFKSDIWAAGCV
 IFELLTLKRTFDATNPLNLCVKIVQIRAMEVDSSQYSLELIQMVSCLDQDPEQRPTAD
 ELLDRPLLKRKRSSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG
 NTHFAVVTVKEKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLOGKAIRQVSCGDDF
 TVCVTDEGQLYAFGSDYYGCMGVDKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVVLT
 NKEVYSWGCGEYGRGLDSEEDYYTPQKVDVPAKALIIIVAVQCGCDGTFLTQSGKVLACG
 LNEFNKLGLNQCMGSIINHEAYHEVPYTTSTFLAKQLSFYKIRTIAPGKTHTAIDERGR
 LLTFGCNKCGQLGVGNYYKRLGINLLGGPLGGKQVIRVSCGDEFTIAATDEKVLNSKTIR
 SNSSGLSIGTVFQSSSPGGGGGGGGGEEEDSQQESETPDPSGGFRGTMEADRGMEGLISP
 TEAMGNSNGASSSCPGLRKELENAEFIPMPDPSPLSAFSESEKDTLPYEELQGLKVA
 SEAPLEHKPQVEASVTELFAPESQLVTSAESCSNLCWEGNTDSSSCVCVQLSAGGG

SEQ ID NO: 233_R86668_H, MKK6_H
 MNLLLSYRDVQDYSAILIELVETLQALPTCDVAEQHNVCFH YTFALNRRNRPGDRAKALSV
 LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYHWYRKAFDVEPSLHSGIN
 AAVLLIAAGQHFEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLGAIILANDPTQV
 VLAAEQLYKLNAPIWYLVSMETFLLYQHFRPTPEPPGGPPRAHFWLHFLQSCQPFKT
 ACAQGDQCLVLVLEMNKVLLPAKLEVRGTDVPVSTVTLSSLEPETQDIPSSWTFPVASICG
 VSASKRDERCCFLYALPPAQDVQLCFPSVGHQCWFGLIQA WVTNPDSTAPAEAEAGAGE
 MLEFDYEYTETGERLVLGKGTYG VVYAGRDRHTRVRIAIKEI PERDSRFSQPLHEEIALH
 RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWG PLKDNESTISFYTRQILQ
 GLGYLHDNHIVHRDIKGDNLINTFSGLLKI SDFGTSKRLAGITPCTETFTGT LQYMAPE
 IIDQGRPGYGKAADIWSLGCTVIEMATGRPPFHELGSPPQAAMFQVGMVKVHPPMPSSLSA

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FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN
STTQSQTFFPCPQAPSQHPPSPPKRCLSYGGTSQLRVPEEPAAEEPASPEESSGLSLLHQE
SKRRAMLAAVLEQELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ
ELRALQGRRLAQGLGPALLHRPLFAFPDAVKQILRKQIRPHWMFVLDSSLRAVRAALG
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR
EILAGKEREYQALVQRALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM
LLNHSFTLHTLLTYATRDDLIYTRIRGGMVCRIWRAILAQRAGSTPVTSGP

SEQ ID NO: 234_PAK6_H

MFGKKKKKIEISGSPNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT
PIQLAPMKTIVRGNKPKETSINGLLEDFDNISVTRSNSLRKESPTPDQAGASSHGPGHA
EENGFITFSQYSSSEDTTADYTTEKYREKSLYGDDLDPYRGSHAAKQNGHVMKMKHGEA
YYSEVKPLKSDFAFASADYHSHLDSLSKPSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA
GTSGCSKESLAYSESEWGPSLDDYDRRPKSSYLNTSPQPTMRQRSRSGSGLQEPMPMPFG
ASAFKTHPQGHSYNSYTYPRLEPTMCIPKVDYDRAQMVLSPPLSGSDTYPRGPAKLQPS
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSQYISTASYLSSLSSSTYPPPSWGSSS
DQQPSRVSHQFRAALQLVVS PGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM
DLRKQQRRELLFNEVVIMRDYHHDNVVDMYSSYLVGDELWVMEFLEGGALTDIVTHTRM
NEEQIATVCLSVLRALSYLHNQGVHRDIKSDSILLTSDGRIKLSDFGFCQVSKVEPKR
KSLVGTPYWMapevisrlpygtevdiwslgimviemidgeppyfnepplqamrrirdslp
PRVKDLHKVSSVLRGFLDMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235_SURTK106_H

MNDRNEIQMEAKLQSLTIIAQEILCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI
LCGPSREGDSPVAMGMTRMLLECSLSCLKCVIQEKQYEVIIIVPTLLVTIFLILLGVILWL
FIREQRTQQQRSGPQGIAPVPPPRDLSEAGHGNNVALPLKETSVENFLGATTPALAKLO
VPREQLSEVLEQICSGSCGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIQF
HQYLGKHKNLVQLEGCCTEKLPYLMVLEDVAQGDLLGFLWTCRRDVMTMDGLLYDLTEKQ
VYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT
IPLKWLAPERLLL RPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKR
PSSCTHTMYSIMKSCWRWREADRPSPRELRLLEAAIKTADDEAVLQVPELVVPELYAAV
AGIRVESLFYNYSML

SEQ ID NO: 236_AA098024_M

LQEKHLFHGDVAARNILIQSDLTPKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL
LRPASIRGDIWSFGILLYEMVTLGAPPYPEVPPTSILQYLQRRKIMKRPSSCSHAMYNIM
KCCWRWSEDSRPLLQVLLQRLLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF
SVL

SEQ ID NO: 237_SGK2ALPHA_H

MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVLAKRKS DGAF
YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE
LFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTD FGL
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVS
QMYENILHQPLQIPGGRTVAACDLLQSLHKKDQQRQLGSKADFLEIKNHVFFSPINWDDL
YHKRLTPFPNPNVTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE
DDDILDC

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FIGURE 1BB

SEQ ID NO: 238_CCRK_H

MDQYCILGRIGEGAHGIVFKAKHVETGEIIALKKVALRRLEDGFPNQALREIKALQEMED
NQYVVQLKAVFPHGGGFVLAFEFMLSDLAEVVRHAQRPLAQAVKSYLQMLLKGVAFCHA
NNIVHRDLKPANLLISASGQLKIADFGLARVFS PDGSRLYTHQVATRSVGCIMGELLNGS
PLFPGKNDIEQLCYVLRILGTPNPQVWPELTELDPY NKISFKEQVPMPL EEVLDPDVSPA
LDLLGQFLLYPPHQRIAASKALLHQYFFTA PLPAHPSELPIQRLGGPAPKAHPGPPHIH
DFHVDRPLEGVAVEPRADSALHPGGVRSWPWSRLPAQDHSVHLFLCHLPGFTLQGLPMA
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239_TESK2_H

MDRSKRNSIAGFPFRVERLEEFEGGGGGEGNVSQVGRVWPSSYRALISAFSRLTRLDDFT
CEKIGSGFFSEVFKVRHRASQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINS
NLEQLLDNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLIKRDENGYS AVVA
DFGLAEKIPDVSMGSEKLAVVGS PFWMapevlRDEPYNEKADVFSYGIILCEI IARIQAD
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLT FNCCNMDPKLRPSFVEIGKTLEEILSRL
QEEERDRKLOPTARGLLEKAPGVKRLSSLD DDKIPHKSPCPRRTIWLRSRSQSDIFSRKP
PRTVSVLDPYYRPRDGAARTPKVNPFSARQDL MGGKIKFFDLPSKSVISLVFDLDAPGPG
TMPLADWQEPLAPPIRRWRSLPGSP EFLHQEACPFVGREESLSDGPPRLSSLKYRVKEI
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEER PAGSTPATF
STSGIGLQTQ GKQDG

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FIGURE 2A

SEQ ID NO: 1_X69117_H BARK2_H

ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC
AAGGCGACCCCGGCCGCCGCGCCAGCAAGAGGATCGTCCTGCCGGAGCCAGTATCCGG
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA
CCTCAGGTGAAGTTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC
CGCCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTTCTTCCTGT
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA
GTGACATCAACTCTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC
ATTTTTCAAAAATTTATGGAAAGTGACAAGTTCACTAGATTTTGTGAGTGGAAAAACGTT
GAATTAAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA
GGATTGGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA
ATCATGTTGTCTCTTGTGACGACAGGAGACTGTCCTTTCATTGTATGTATGACCTATGCC
TTCCATACCCAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTGTCAC
TACCACCTTTCAACACCGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA
ATCATTCTGGGTCTGGAACACGTGCACAATCGGTTTGTGTTCTACAGAGATTTGAAGCCA
GCAAATATTCTCTTGGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCTGC
GATTTTTCCAAAAAGAAGCCTCATGCGAGTGTGGCACCCATGGGTACATGGCTCCCGAG
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGGCGACTGGTTCTCCCTGGGCTGCATG
CTTTTCAAACCTTCTGAGAGGTCACAGCCCTTTTCAGACAACATAAAACCAAAGACAAGCAT
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACCTCCAGACACCTTCTCTCCTGAA
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTCAC
GGAGGCGGCTCACAGGAAGTAAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT
GTCTACTTACAAAAGTACCCACCACCTTGATTCTCCCCGGGGAGAAGTCAATGCTGCT
GATGCCCTTTGATATTGGCTCATTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTCATCTCTGAACGCTGGCAGCAAGAA
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT
ATGCACGGGTACATGCTGAAACTGGGAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT
TTTACCTCTTTCCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAATGCATT
TTGTTTCAATAAAAGGAGGGAAACAATTTGTCTTGAATGTGAGAGTGATCCAGAGTTT
GTGCAGTGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCGT
GCCCCGAAGTTCTCAACAAACCTCGGTACAGGTACTGTGGAGCTCCCAAAGCCATCCCTC
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2_AA144574_M BARK2_M

CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA
CGTGAGGATATCGGATCTCGGCCTTGCTGTGATTTCTCCAAAAAGAAGCCTCATGCCAG
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAAACGTGCTATGACAG
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCGTGACCGTGAA
CGTGCAGCTTCCAGATGCCTTCTCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGAGAGCATCTATGACGCCGTCAA
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

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FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTACCTGTTCCCCAACAGACTGGAGTG
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTACTCAGGATAAAGGGAGGGAAGCAATT
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC
CTTCAATGAGGCCCAGAGACTGCTGCGCCGTGCCCCCAAATTCCTCAACAAACCACGGGC
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTACAGAAATAGCAGCGGCCTCTGAAC
CACAGAGCAGCGGGCCCTGAAGGAGGGGCCCCAGCTCTTCAGCCCAGGAGTGGAACGAAG
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTCTCTGAGCACTGACGGGGCTGCTCCA
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3_AA826850_H

GAAGAGGATGGGCTCGTCCATGTGCGCGGCCACCGCGCGGAGGCCGGTGTGTTGACGACAA
GGAGGACGTGAACTTCGACCACTTCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG
CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCGGGAGCTGGAGATCCT
GCAGGAGATCGAGCACGTCTTCTGGTGAACCTCTGGTACTCCTTCAGGACGAGGAGGA
CATGTTTCATGGTCTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA
CGTGCACTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT
TGTCAACGGCGGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTCCGGTGGGGGTGATGGC
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC
CCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGTGTGGGACCACCTGAGCGAGAAGAG
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTCTGCACTGCGACCCACCTTTGAGCT
GGAGGAGATGATCCTGGAGTCCAGGCCCCCTGCACAAGAAGAAGAAGCGCTGGCCAAGAA
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTAAACAGAGAAAAGCTGAAGAGGAGCCA
GGACCTCCCGAGGGAGCCTCTCCCCGCCCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCATTTGCCCTCGGCCGGGAG
CGGCTAGGCCGGGATGCCCGTGGTCTTCAACCTTGAGCTGCTTTGGAGACTCGGCTGCC
AGAGGGAGGGCCATGGGCCGAGGCCTGGCATTACGTTCCACCCAGCCTGGCTGGCGGT
GCCCCAGTGCCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCTGGTGGGCCCCGAGACCCGCCTA
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGAGCTGGGGCCATGGATG
GGACAGGAGTCTTTGTCCCTGCTCAGCCCGGAGGCTGTGCACGGCCCTCGTCACAAGGTG
ACCTTTCAGCACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGAGGTCAGGGGC
ATGGGTTGGGGTAGTGGGTGGGAGGTGAATGTTTTCTAGAGATTCAAACCTGCTCCAGCA
ATTTCTGTATAGTTTTACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4_AA960957_H

GTCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG
GAATATGGCGGGGAACCACTCCACAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA
CTTTGACATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT
CGTGAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG
CATCGAGAGGGATGAGGTTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

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FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTTCATGGT
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTAC
AGAGGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG
GTACCACATCATCCACAGAGACATCAAGCCAGACAAATATCCTGCTGGATGAACACGGACA
TGTTTCATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAAGGGCTTCCTC
CATGGCTGGCACCAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG
CCCCGGATACTCGTACCCTGTGCGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCCATCGATGAAATCCTCAACAT
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGAT
TCTAGAATCCAAGCCACTTCACAAAAAGAAGCGATTGGCAAAGAACAGATCCAGGGA
TGGCACAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA
GCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCACACTTG
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCTCTTTGTGC
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGA
GCTGGGAAGCCTGGGTCTGGTCCCATCTCCATGACTGATTACGTGTGACCTCAGACAA
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTAAACACTTCTGCC
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT
TGATATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC
ATTCCCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA
GGGCACTTCCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCCCTT
CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT
CTGGCAGGCCACAGTCCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCCTCATTTAAGAAGACTATCCTTACCTTTT
AGTTTCAGCAGTCCTCACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA
TTCAGATGAGAGTTGGGTGCGTGAAGATTGGTTACTCCTGCAGAGTGTAATCAGCACCCC
ATCCAACCTGGCCCGAAAGGCCAGACCTGCAGCAGAACTCTCCAACCTCTCTATCAGCTTTC
AGGGTTTTCTCTCCTGGGAAGGGTGTAATAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG
AAAGTTTATTTTCAAGGAGGAAAATGGGTTTACACAAAAAGCAAACCTACATTCTGATCTGCT
CAGGGAGAAGCTTGCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGGAAAGCTTAGACTT
TGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAACTAACTGGGAGACCTT
AGGCAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTTAAACAGGGATAATAAA
ACTAATATTGCAAGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG
GATGACTCATAGAATGGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTC
TTCCTTCACTCACCCAGCAGGTGAGTTTTCTGTGCAACAAACCTGTTTAGGATTCTTCC
AAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTGTTACATCCTGCTGAAGTTCGACTGTG
TTTTTATTTTTTTCATCCAACCTCCATTTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCTCTTAGATTTCTTAAAAGACATTTTAATGTATGGTTAGGTTTTAT
ATTTTTATTTTTTAAAAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTT
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTGTTTGCACTTTTCTTTACTTCATGTCCC
CATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGCCTGCTCCTCTCCCT
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGA
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTCTGTTCAGT
TGGCATTCTTGTGTTGGAATAAACTATTTCTTGGACATTCCTTC

FIGURE 2D

SEQ ID NO: 5_TBK1_H

TCCTGAGTCTCGAGGAGGCCGCGGGAGCCCCGCCGGCGGTGGCGCGGCGGAGACCCGGCTG
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG
ATGTTCAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTTGTC
CATGTGGGAGTTTATACACTGTTTTAGAAGAACCTTCTAATGCCTATGGACTACCAGAAT
CTGAATTCCTTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCACTCTTT
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG
AAAAGTGTTGGGGTTTTGACCAGTTTTTTGCAGAACTAGTGATATACTTCACCGAATGG
TAATTCATGTTTTTTTCGTACAACAAATGACAGCTCATAAGATTTATATTCATAGCTATA
ATACTGCTACTATATTTTATGAAGTGGTATATAAACAACCAAAATATTTCTTCAAATC
AAGAACTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT
TCCCTAAACTACTGAGGAAAACCTATATTTGTAGTAAGCCGGGAACCTCTGAATACCA
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA
TTAAAGATGATTACAATGAACTGTTCACAAAAAGACAGAAGTTGTGATCACATTGGATT
TCTGTATCAGAAACATTGAAAAAAGTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC
TGGAAGCGGCAGAGTTAGGTGAAATTTAGACATACACACCAAATTTGTTGAGACTTTCCA
GTTCTCAGGGAACAATAGAAACAGTCTTCAGGATATCGACAGCAGATTATCTCCAGGTG
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG
AAAACTACAAGTCCTGTTAAATTTGCATGACAGAGATTTACTATCAGTTCAAAAAAGACA
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAATCCACAAATTTGATAAGCAAAAAAC
TGTATTACCATGCCACAAAAGCTATGACGCACCTTTACAGATGAATGTGTTAAAAAGTATG
AGGCATTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT
TATTATCGCTGACTAATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAT
ATACTAATGAGTTACAAGAACTCTGCCTCAGAAAATGTTTACAGCTTCCAGTGGAATCA
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGTA
TGAAGAAAATTAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA
TTTTAGAAAAGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT
AGCTTTCTAATAGAAGTTTAAGAAAAGTTTCCGTTTGCAAGAAAATAACGCTTGGGCA
TTAAATGAATGCCTTTATAGATAGTCACTTGTTTCTACAATCCAGTATTTGATGTGGTCG
TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTTGGCTGCTGTGAA
GATGTAATTTTATCTTTTAAATTTATAATTATATGAGGAATTTGACCTCAGTGATCAC
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC
TAAATAAGTTATTTTCTCTGACCGCTACTGGAAATATTTTAAAGTGGAACCAAAATAGG
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAAATGGTAGAACGGTGGCTAC
TGTGAGTGGGGAGCAGAACCGCACCACTGTTATACTGGGATAACAATTTTTTTGAGAAGG
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCAGATCCCAGTTATCCTTGTATCCATG
TAATTTTCAAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTA AAAACTATTC
ATTTTTTTTCTTTGGCCATAAATGTGTAATTGTCAATTA AAAATTC TAAGGTCAATTTCAACT

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FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT
CAATTTTAAAAAA

SEQ ID NO: 6_AA305176_H

TGGCTGCTCGCGGAGGGGCGAGTGTACGCGGGGCGGCTGTAGGCTGTCCAGCGATGGATCC
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGGCGGCGACTGAGGAGGGCGTGAATAG
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATTAGCCG
GGGCGCCTTCGGGAAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT
TGTTAAAAAAGCAGACATGATCAACAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA
TGCCTGGCACTAAGCAAAAAGCCCATTCATTGTCCATTTGTATTATTCACTGCAGTCTGC
AAACAATGTCTACTTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT
TATTTCTAATGAGGGTCATATTAACTGACGGATTTTGGCCTTTCAAAGTTACTTTGAA
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA
TTATTCAAGAACCCAGGACAAGTGTATCGCTTATCAGCTCGTTGGGATTTAACACACC
AATTGCAGAAAAAATCAAGACCCTGCAACATCCTTTCAGCCTGTCTGTCTGAAACATC
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCCTTA
TTCTAGCAAATTACTAAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG
TAGTCAATCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCATAAAGAAATGAAATTGTTA
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCCTGCACATTCTGTCAAATTC
TTTTGAAATATTTTCATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA
GATTCCTTGCAATAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTTGGTTTTGTTTTATTTTGT
TTTTAACATATGTCATTTAAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7_AA116841_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG
CAATGGACATGCTTTTAACCATTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAC
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTTCG
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCAATTTTATCTAATTGTGA
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAATTACTAAGTACAACAGTTTTTACAG
AATTAATACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAACTGTATATAA
GCCATAATAGCTTTTTTTCATCTTATTTATTCACTGCACTTTATGAAGAGCAAAGTATCAA
TAACTAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8_AA256100_H

AGGGAGCTGACGGGCGCCCGGCCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC
TATGAGCAACCATAACCCGGGAAAGAGTGACTGTAGCCAAGCTCACATTGGAGAATTTTAA
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATTAGAAGTGGC
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTCGATCACAACACGCTCG
CAAAGAAACAGAGTTCTTACGGCTCAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

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FIGURE 2F

GGCCCATATCCGAGCAGAAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA
GATGTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT
CTACATTTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTTCATCCATCG
GGATATTAAGCCAGACAACCTTTTATTGGATGCCAAGGGTCATGTAAAATTATCTGATTT
TGGTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA
CAACCCACCAAGTGACTTCTCATTTCAGAACATGAACTCAAAGAGGAAAGCAGAAACTTG
GAAGAAGAACAGGAGACAACCTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC
AGAAGTATTTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA
CAGAAAAGTGATGAACTGGAAAAGAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA
GAAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAG
TGGAGTAGAAGAAATAAAAGGTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA
TGACTTCCCTGAATCTGATATTTTACAACCAAGTGCCAAATACCACAGAACCGGACTACAA
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC
TGAAATACTCCTGAAGATGGTGGTGCCTTATTGACTACAAGAGGAAATTCACAGGATTAG
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAATAT
TTTATTATTTTTGTTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT
TTGAACTGTAACACCTCTAATCAATTCAAGGAGAAACACATATCATTTAAAGCAACATAGG
CTAACCTGTAGGTAACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTTAGAACATTGCCCTATTGGTTTGGACATC
TGTAAGATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAGAAATTC
CTGTTCTTTTACAAAATAGAATTTATCATCAAGTTATTACACAACTTCACAGTAAGGAG
TGACAAGTTTTATAATAAGGAAGACAAAGTTTTAACACCTTCACTCAAGCACTCCACTAATA
TATTTACGTTGCATTTCAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGAACTTCTT
TTTTTAACAAGAGGACATGGCATTATTTTAATTTGATTATGGTGAGTTGAATTTAAGACA
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTTATTAACTATTTTTTTAAATGTC
AACTTCTATCATGTAAATGGACTTATAGAGAACAAAAAGCTATTTACTTTGGTTTTCTA
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTTCTTTTGATGAAAATTTTCTCTT
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAAGATCTT
GAACAGAGTGATGTTCACACTGAGTAGAATTTTCTTTTCTGTGGGCATGCTGTATTTC
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAAGGGCAATATTGTTCTTGTGTTAG
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGTTGT
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATCTTTGGGTATCTCTCTAAGAATT
AAATAATCTTTTCTAGCTTAATATTTTAATTCTAATTCAAACAACCTCTGAGGTTTGGTT
TCATTAGTAATAGTTGAGGAATAATACTAGCAAAGAATGGCCTAATGTTTGTCTATAAC
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATATAAATGATCTATGA
TCAAAATCTAAAGTGATGAATTATTTGTAGGAATGTCTTCTAATGGGGAAGAATTGCAT
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG
TGTTTCATAAGGCCATCCTGTTCCCCCACTCCCCATTTTGGTTTGTCTTTTAA
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACTTCCATTTTCTAGTCTGGAT
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAACTCTGGGGATTCTCAATGTGACTAA
CTCTAATTTTTCTAATTATACTGCCTTTAATTAAACATAATATTAACTTTTGCTGAGGTT
TATGAGATTTTCTACCCCACTCGCTCCCTTTTTTAAAAGGACTGTTTTGCTAGTG
TGATAATGAATAGGTAAAGATATGAGATAATTGCAACATTGTCCTAGTTCTAGTATGGTAA

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FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA
GAAACTGATTTACCTAAGTTTACTTTTAAATTGCATAATAGAGCATTTTTTGTGAGT
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTACTTTCTTGGCACTGGAAG
GGTAGTTCTGGAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAGCATTCTTAAGTGCCTATCTAAAAGC
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTCATGATGCAAATTA
AGATAATTTGCAAAGTACCCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTT
AGGTGAATAATTTAATTTAAATGACAAAACCCCTATCTAGTCAACTGGGCATAATGACATT
TTCTTTAAATTAGACTCTATTTGAATTAAAAGAGTTTTATTATAAACCGTGTGTTTTG
GTTTTTCTAAGTATATAGAAAGCTTGATAATTCAGATTTATCAATTTCCCTGATTAAATG
TAGACTTTGACTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT
GAAAAATAAGGAATTGCTTATAAACCCAGCCACTTCTGAATACAATATGTAGCTGATTAAAT
AAGCTAGTTAGTGAATGGAAAAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT
TTTATGTAAATCTCTAAATTTAAATATTTTAAAGTACATTTATTTTTGGTGTGTTTTATTGT
ATAAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA
ACACATTCTCCTTTGAATTGTTAAAATTCAGAACATTCAAATAACTGTTTTGCTACAAC
CCATGATTATTTTCTGTTGTGTTTATTTAAATTTACTTTCTCTTTAGAAGTGCATTAT
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA
CTACTAGAGATATTTTAGATTTTATGAAAAAATGTGAGGGGATATTGCTGCTTTAAAA
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTCAGCAAT
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTCAGTTACTGAGTTTCAAAAA
TGTTTTGGTGGCATGAGGACAAAATTTCAATTGAAGGTAAGATAAGAATAAAAACTATGTT
TAC

SEQ ID NO: 9_AA210825_H

CACGAGGGCTACTGGCGCCTGGCGACCCTCCCTGCCCCCACCACCCCGCTCCGGCAA
CGCCCCCTTCTCACGGCTCCCGACCGAATTTTCTCCAACTTCTGCGACTCGTGAGATT
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCCTGGCCGGTCCGGTCCC
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA
CCCCCAAGGACCCCGCCATCCTCAGGTCCCTCCGCCTGCCAGATCTTTTCTCGGATCCC
CGCTCTCCACACCTGCTCACGAGATCCCGCGGATCTAGAACCAGGGTCCCCCGGGGC
CCCCCGGCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCCTCCCCCATGGCCAC
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGGTCTCCTCCGCCCC
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCCGGGTT
CCGGGGTCTCCTTTACATCCAGATCGGGCTGACCCGCGAGTTCTGTCTGTTGCCCGCCG
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGGACCAGAAGTTCCTTG
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCACGTCGG
CCAACCTCCTGCAGCTGGTGCCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG
TGGTGTGTGCGCCTCGGCCACCTTCGAGGACTTCAGATCCGCCCCGACGCCCTCACGG
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG
TGCGCCAGGGCCTCAAGTGCGATGGCTGCGGGCTGAACTACCACAAGCGCTGTGCCCTCA
GCATCCCCAACAACTGTAGTGGGGCCCCGAAACGGCGCCTGTCTATCCACGTCTCTGGCCA
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA
GCCGTAGCACCACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCTCCTCTTCTG
CCTCATCGTATACGGGCCGCCCCATTGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG
TGCCGCACACCTTCTCATCCACAGCTATACACGGCCCCACCGTTTGCCAGGCTTGCAAGA
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGTT
GGGTGGTTTCATTACAGCAACAAGGACACGCTGAGAAAGCGGCACTATTGGCGCCTGGACT
GCAAGTGTATCAGCTCTTCCAGAACAACACGACCAACAGATACTATAAGGAAATTCGCGC
TGTCAGAAATCCTCACGGTGGAGTCCGCCAGAACTTCAGCCTTGTGCGCGCGGGCACCA
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG
GCGGGACTCCGGGTGGGCCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA
CAGCCATCCGCCAGGCCCTGATGCGCGTTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGGGACGTGGCAGTTAAGGTCA
TTGACAAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTTC
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTTCGAGACGCCTGAGA
AAGTGTGTTGTGGTATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG
AGAAGGGCCGGCTGCCTGAGCGCCTCACCAGTTTCTCATCACCAGATCCTGGTGGCTT
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC
TGGCATCAGCAGACCCATTTCCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA
TCGGCGAGAAAGTCTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGGCGTGATCATGT
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC
AGAACGCCGCCTTCATGTACCCGGCCAGCCCCTGGAGCCACATCTCAGCTGGAGCCATTG
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA
AGATGGGAGAGCGATACATCAGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCACGGACAGGGATCTCGGTGGGGCCTGTC
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTCTCTGAGGTCTTG
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGTTCTTTCACAGGATCCCAGCAATGAACTG
TTCTAGGGAAAGTGGCTTCTGCCCCAACTGGATGGGACACGTGGGGAGTGGGGTGGGGG
GAGCTATTTTCAAGGCCCCCTCCCTGTTTCCCCAGCAATTAAAACGGACTCATCTCTGGCC
CCATGGCCTTGATCTCAGCAAAA

SEQ ID NO: 10_AA127299_H

ATTCAATTCAATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT
GATCCTTACATCAAAATCACAAATCTTTCTCAAAAAACGAAAGTGATTAAGAAAACCTTG
ACTCCAACCTTGGAATGAAACTTTTTTTGTGCATTTTCCAGAAAAACAACCTTGAATTA
GAATGTTGGGACCACGATACTTTTTTCAGATGATTTTATTGGCAAGGCTTCCATTTCTTTG
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAAGGA
GAATTTGCAGGAAAA

SEQ ID NO: 11_AA316804_H

ATGTCGTGCAATAATTCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCCT
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCCTAAGACGGGACTCTCTGCCCGACTC
TCTAATGGAAGCTTCAGTGCACCATCACTACCAACTCCAGAGGCTCAGTGCATACAGTT
TCATTTCTACTGCAAAATTGGCCTCACACGGGAGAGTGTACCATTGAAGCCCAGGAACTG
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT
GGATTCTTTGGCATGTATGACAAAATCTTCTCTTTTCGCATGACATGAACTCAGAAAAC
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

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FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTTCGTCCACATACTCTCTATGTACAT
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT
CAAGGACTGAAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT
CCAAATAACTGTAGTGGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA
CATGTCCACCAGGAACCAAGTAAGAGAATTCTTCTTGGAGTGGTGCGCCAATCTGGATG
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG
CAGTGTAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAAGTACCAAGAGAC
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCTTCCAGTCTGGGAACAGATACAGATATA
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAAATGGTGAAGGAA
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT
GACAGCAAATGTCTAACATTATTTTCAAGATGAATCTGGATCAAAGTATTATAAGGAAATT
CCACTTTTCAAGAAATTTCTCCGCATATCTTACCACGAGATTTTCAAAAACATTTTCAAGGC
AGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATACTTCGTTGGTGAGAAC
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA
CAGAGCTGGGAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT
TGCACTTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT
AATTGTGAGATTGAGGAGAAATGTGGATATCAGTACTGTTTACCAGATCTTTCAGATGAG
GTGCTTGGTTGAGGCCAGTTTGGCATCGTTTATGGAGGAAAACATAGAAAGACTGGGAGG
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT
ATGTTTGAACCCCAAGACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG
GAAATGATTCTATCCAGTGAGAAAAGTCCGCTTCCAGAACGAATTACTAAATTCATGGTC
ACACAGATACTTGTGCTTTGAGGAATCTGCATTTTAAGAATATTGTGCACTGTGATTTA
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCTCAGGTGAAGCTGTGTGAC
TTTGGATTTGCACGCATCATTTGGTGAAAAGTCATTGAGGAGATCTGTGGTAGGAACCTCA
GCATACTTAGCCCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCTTTTAAATGAGGATGAA
GATATAAATGACCAAATCCAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA
ATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC
CTTAGAGAATTTGAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGATGCT
CGCTGGGAAATACATGCATACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT
CCTAATCCAGATGATATGGAAGAAGATCCTTAA

SEQ ID NO: 12_PKNBETA_H

ATGGAGGAGGGGGCGCCGCGGCAGCCTGGGCGGAGCCAGTGGCCCCCAGAGGATGAGAAG
GAGGTGATCCGCCGGGCCATCCAGAAAGAGCTGAAGATCAAGGAGGGGGTGGAGAACCTG
CGGCGCGTGGCCACAGACCGCCGCACTTGGGCCATGTGCAGCAGCTGCTGCGGTCTCTCC
AACCGCCGCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCCGAATCCTGCTG
CCCGGCCCTGGGCTGGCCAGCTGAGCCTGTGGCCTCAGGACCCCGGCCGTGGGCAGAG
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCCAAGGAGAGGAAG
CTCCTTGCAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGAGCCAGGGCCTGAGCTACTGGCG
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAAGCTG

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FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCAGGCC
CAGCTACAGGAGTCCTCTCAGAACTGGACCTCCTGCGCCTGGCCTTGAGCAGCTGCTG
GAGCAACTGCCTCCTGCCCCACCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCCCACCGCCCTAACAGGGACA
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA
GCGGCCGCACTGGCCAGCAGCCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT
GTGGGGCAGACGGGCTGGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTCATC
CCACTGGAGCGAGCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA
TGTGGCGTGGCCTTCCTGAGACTTGAAGACTTCCTGGACAATGCCTGTCACCAACTGTCC
CTCAGCCTGGTACCGCAGGGACTGCTTTTTGCCCCAGGTGACCTTCTGCGATCCTGTATT
GAGAGGCGGCCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC
TTCCTGAGGCGTTTCGCAGATGAACCTCGGCATGGCGGCCCTGGGGGCGCCTCGTCATGAAC
CTGCTGCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCTAAAGGATGCCCTCGGACC
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCCAGTAATTTCTGCCCCAAGAAG
ACCCCTTTGGGTGAAGAGATGACACCCCCACCAAGCCCCCACGCCTTACCTCCCCCAG
GAGCCAACATCCGAGGAGACTCCGCGCACCAACCGTCCCCATATGGAGCCTAGGACTCGA
CGTGGGCCATCTCCACCAGCCTCCCCCACCAGGAAACCCCTCGGCTTCAGGACTTCCGC
TGCTTAGCTGTGCTGGGCGGGGACACTTTGGGAAGGTCTCTGGTCCAGTTCAAGGGG
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCTT
TTCCTGCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCCGCTTTGTGACTGAG
TTTGTGCTGCTGGTGACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG
GCCCCGCTTCTACGTGGCTTGTGTTGTCTGGGGCTGCAGTTCTTACACGAGAAGAAGATC
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCCAGGGATTCTGAAGATC
GCAGACTTTGGACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT
GGCACCCCCGAGTTCCTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACAGGCCGTC
GACTGGTGGGCGCTGGGTGTGCTGCTTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA
GGGGACACAGAGGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCCGGC
TTTCTGTGCGTGCAAGGGCTTGAGTTCATTTCAGAAGCTCCTCCAGAAGTGCCCGGAGAAG
CGCCTCGGGGCAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC
ACCAACTGGCAAGCCCCTGCTCGCCCCGACCATCCAGCCCCCTTCGTGCCTACCCTGTGT
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTCACAGGGCTGCCGCTGCCCTGACC
CCACCTGCACCCACAGCCTCCTCACTGCCCCGCAACAGGCCGCTTCCGGGACTTCGAC
TTTGTGTGACAGCGATTCTGGAACCCTGA

SEQ ID NO: 13_AI021023_M_PKNBETA_M

GCTGAAGTGGGATAACCTTCTGCTGGATGCCCAGGGATTCTGAAGATCGCAGACTTTGG
ACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGTGGCACCCCGGA
GTTCTTGCTGCCGAGGTGCTGACCCAGGAGGCATACACACGGGCTGTGGACTGGTGGGG
GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA
GGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCCGGCTTTCTGTGCGT
GCAAGGGCTTGAGTTCATTTCAGAAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGGC
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA
AGCCCTGCTCGCCCCGACCATCCAGCCCCCTTTGTGCTTACCCTGTGTGGCCCTGCGGA
CCTGCGCTACTTTGAGGGCGAGTTCACAGGGCTGCCGCTGCCCTGACCCACCTGCACC
CCACAGCCTCCTCACTGCCCCGCAACAGGCCGCTTCCGGGACTTCGACTTTGTGTGACAG
GCGATTCTGGAACCTGAGGGCATCTCCTGGCACCTCTGTCCCTTCCCCACAGACTG
TTAGAGCCTCTGCTCGTTACCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

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FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA
GACCTGGCCCAGAAAGGGTGCCGCAGCAAGGAGTGATATGGTTTGTCTTTTAAAGACTGG
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14_H19102_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA
ACCATCAGGTCAGATCTGGAAGAACTCTGGGAACTACGGGGGCACCACTATCTGCACCAG
GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGGCCAGTGCCT
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG
CTGAAGATTTTAGGCCTCGTGGCTAAAGGCTCCTTTGGAAGTGTCTCAAGGTGCTAGAT
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCAAGGTAAAGGTCCCTACAGAGG
GATACCGTGAGGCAGTGCAAAGAGGAGGTTAGCATCCAGCGACAGATCAACCATCCCTTT
GTACACAGCTTGGGGGACAGCTGGCAGGGAAAACGGCACCTTTTTCATTATGTGTAGCTAC
TGCAGCACAGATCTGTACTCCCTTTGGTGGGCTGTGGCTGCTTTTCTGAGGCTTCCATC
CGTCTCTTTGCTGCCGAGTTGGTGTGGTACTGTGTTATCTCCATGACTTGGGCATCATG
CATCGAGATGTGAAGATGGAGAATATTCTTCTAGATGAACGAGGCCATCTGAAACTGACA
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT
CTTCAGTACATGGCCCCAGAGGTCTTAAGTGGAGGACCTTACAACCATGTGCTGATTGG
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGGCGACTGGAAAGTTTCCAGTGGCTGCAGAG
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGAAGTCTGAGATCCCAGCTTCT
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCTCCATCGT
CTACGTTATCTGCATCACTTCCAGGTCCACCCCTTCTTTTGGGGTGTGGCCTTCGACCCA
GAGCTCCTACAGAAGCAGCCAGTGAAGTTTGTACGGAGACACAAGCTACCCAGCCCAGT
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC
CCTATCCCTGCTTGA

SEQ ID NO: 15_AA476563_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAAGTCTCTGGGACTTGACTTT
GGAGAAAAATGTATAGTCTAAAATCAGAACCTTTGAAACCATTCTTTACTCTTCAGAT
GGAGACAGTGCTTCTAGGAGTTTTAATACTAGTGAAAGCAAGGTAGAGTTTAAAGCTCAG
GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTTCGTTTAAAGATGCTGCT
TTTGATGATGTGAGTGGTACTGATGAAGGAAGACCTGATCTTCTTGTAATTTACCTGGT
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAACTAAT
ATAGGGATAATAGAAAAATAAAGTCTTGGAAAGCCCCCTGATGTTTTATGCCTCAGGCTTAGT
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAAGTGAAGTATCCCTCTGGG
CCCAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT
GTAGCAGCTGTTGATCATAGTAGTTTCAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
TTATTCCGTATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTTGGCTAAAGAGGAA
CCAATTCTTTATTCCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA
GGAGACAAGGAAATACATCAGATTTTGGAGACCTTGATAAAAAATTAGCACTAGCCTCC
AGGTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT
GATGCTTTACATAGAGAGGGAATTGTGTGCCGCGATTGTAACCCAAACAACATCTTATTG
AATGATAGAGGACACATTCAAGTATTTTAGCAGGTGGAGTGAAGTGAAGTGAAGTGAAGT
TGTGACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTTGGAGCAATCACTGAA
GAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCCTCTTTGAAGTCTCACTGGC
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATCAACAGCTCTTGCAAGTTCATCTCTG

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FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTGAAGATATCAAATCTCATCCATTTTTTACC
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16_AA626690_H

ATGCTACCATTGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTTCAGCGGC
GGCGGCGCGAGCAGCGGCGAGGTAAATGGTCTTAAATGGTTGATGAGCCAATGGAAGAG
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT
CAGGGGTCATTTGGAAGGTTTTTCTTGTTAGAAAGAAGACCGGTCCTGATGCTGGGCAG
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTAAAGTTTCGAGACAGAGTTCCGGACA
AAGATGGAGAGGGATATACTGGTGGAAAGTAAATCATCCATTTATTGTCAAATTGCACTAT
GCCTTTCAGACTGAAGGGAACTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATTCTACCTCGCA
GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTTGGTACAGTAGAGTATATG
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCAGAGTGCTGATTGGTGGTCATATGGT
GTTCTTATGTTTGAAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG
ACCATGAATATGATATTAAAGCAAACCTTGAATGCCTCAATTTCTTAGTGCTGAAGCA
CAAAGTCTTCTAAGGATGTTATTCAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA
GTTGAAGAAATCAAAGACATCTGTTTTTTTGCAAATATTGACTGGGATAAATTATATAAA
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGAAAACAGATGATACTTTTTGTTTT
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGTTTTGCCAGCCAGTGCAAT
GCTCATCAGCTCTTCAAAGGATTTCAGCTTTGTTGCAACTTCTATTGCAGAAGATATAAA
ATCACTCCTATCACAAGTGCAATGTATTACCAATTGTTTCAGATAAATGGAAATGCTGCA
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGGCTCCTACTCTGTTTGC
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAAATGTTTCTCGGAACGGGAGGCT
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGCAAGATTCA
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACCTTCGAGGAGAAAATGGACTTCTCTTA
ACTCCATGCTACACTGCAAACTTTGTTGCACCTGAGGTTCTTATGCAACAGGGATATGAT
GCTGCTTGATATCTGGAGTTTAGGAGTCTTTTTTACACAATGTTGGCTGGCTACACT
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA
AAATTCTCTTTGAGTGGTGGAACTGGGACAATATTTCAAGCGGAGCAAAGGATTTGCTT
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA
CCAGTCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCCAGCGACGGAGCATGAAAAAGCGA
ACATCAACTGGCCTGTAA

SEQ ID NO: 17_AA215680_H

ATGAGCCTGGTGGCCTGTGAGTGCCTGCCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTGCAACAGGGTGGCTCTGGGA
GTGCCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC
CTGGAGCGGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG
GACGTGCTGCTCCGTGGCATAACGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG
CTGAAAATTACCAAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

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FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGCGGGTTTCAGCAGCCTGAGGCTCCGGCCCAT
CGCAGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCCGGGTCATCGAG
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC
AGGTGCCACATGGTGAAGCAGGGAGCGGCTGACCATCATCCACACGGAGTCCCTACATG
ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCCTGCACCTGGAGCATGTG
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG
ACCCAGCGAGGCTTCCCTCAGGCCATGCCCCTGGCCAGGACAGAATCGCCCTGGAGCCT
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACCAGACCCAGAGG
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG
GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG
CCCCCTCGGGGGCTCACTTGGGTTCTGAGGGGGCCGGCCCGGTGCTAGGGGGCTGTGGC
CGAGGCATGGATCAGAGCTGCCTGTGAGCAGATGGGGCCGGCCGGGGCTGTGGCAGGGCC
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG
GAGGCGCTGCACGAGCAGGGGGTGTGTGCCGGGACCTCCACCCCGGAACCTGCTCCTG
GACCAGGCAGGTACATCCGGCTCACATATTTGGCCAGTGGTCAGAGGTGGAGCCCCAG
TGCTGCCGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAAGTCTGACGGGA
ATGGCACTGTCCCAGAGCCACCCTTCAGGAATCCAGGCCCACACCCAGCTCCAGCTGCCC
GAGTGGCTCAGTCGCCCAGCGGCTCTCTGCTGACTGAGCTGCTGCAGTTCGAGCCTACC
CGGCGCTGGGCATGGGAGAAGGTGGTGTGAGCAAACTCAAGTCCCATCCCTTTTTTCAGT
ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18_SGK_H

ATGACGGTGAAAACCTGAGGCTGCTAAGGGCACCCCTCACTTACTCCAGGATGAGGGGCATG
GTGGCAATTCTCATCGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAG
AAGATTGCCAATAACTCCTATGCATGCAACACCCTGAAGTTCAGTCCATCTTGAAGATC
TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCCTTCT
CAGCAAAATCAACCTTGGCCCCGTGCTCCAATCCTCATGCTAAACCATCTGACTTTCACTTC
TTGAAAGTGATCGGAAAGGGCAGTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCAGAA
GAAGTGTTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG
AAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTTCTGGTG
GGCCTTCACTTCTCTTTCCAGACTGCTGACAAATTGTACTTTGTCTTAGACTACATTAAT
GGTGGAGAGTTGTTCTACCATCTCCAGAGGGGAACGCTGCTTCTGGAACCACGGGCTCGT
TTCTATGCTGCTGAAATAGCCAGTGCCCTGGGGCTACCTGCATTCACTGAACATCGTTTAT
AGAGACTTAAAACCAGAGAATATTTTGCTAGATTACAGGGACACATTGTCTTACTGAT
TTCCGACTCTGCAAGGAGAACATTGAACACAACAGCACAAATCCACCTTCTGTGGCACG
CCGGAGTATCTCGCACCTGAGGTGCTTATAAGCAGCCTTATGACAGGACTGTGGACTGG
TGGTGCTGGGAGCTGTCTTGATGAGATGCTGTATGGCCTGCCGCTTTTTATAGCCGA
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAATATT
ACAAATTCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTCCTTAATTAAGTGG
GATGATCTCATTAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCCCAAC
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTGGCAAG
TCCCTTGACAGCGTCTCGTACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCCTAGGC
TTTTCTATGCGCTCCACGGACTCTTTCCTCTGA

SEQ ID NO: 19_AA107515_M

CGGGTCGACCCACGCGTCCGCCGGTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCCCTTACCTACTCCA

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[illegible]

CCACCTGCAGCGGGAGCGCCGGTTCCTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGT
GGCCAGCGCTTATTGGCTACCTGCACCTCCCTCAACATCATTTACAGGGATCTGAAACCAGG
GAACATTCTCTTGGACTGCCAGGGACACGTGGTGCTGACGGATTTTGGCCTCTGCAAGGA
AGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACCCCTGAGTACTTGGCCACC
TGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGCTTGGGGGCAGT
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCCAGATGTA
TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGGACAGTGGCCGCCCTGTGA
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTT
TCTTGAGATTAAGAACCATGTATTCTTCAGCCCCATAAACTGGGATGACCTGTACCACAA

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FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGA
CCCAGAGTTTACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC
CAGCAGCTCTGGGGCCTCAAGTGCATTCTGGGATTTTCTTATGCGCCAGAGGATGATGA
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAAACTACTGAGGCCAGCTGGTATTAGTA
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAAC TAACAATGGCTTCAACGAGAAG
CAGGTTTATTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT
CCAATGTTAGGTTTGCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAG
GGAAGGGAAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAA
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTT
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG
CCTCCTGGTGTGTTGGATTTTGATCTCAATGTGTAAAATGACAGAGATGTAACAAGCTCAT
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21_AA887783_H

CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT
ACAAGGAAAGCTGCCCAAGTGTAAGNATCCAGCTCCGATGAACACAGAGAGAAAAAGA
AGAGGTTTACTGTTTATAAAGTTCTGGTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAACAGTTTCTGCTANGG
CCCTGAAGATTCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAAC
AAAGACGAGCAGGACTAAACGAATTCATTGAGAACCTAGTTAGGTATCCAGAACTTTATA
ACCATCCAGATGTCAGAGCATTCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCAT
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAACATCAACC
TGGGACCGTCTGGAAATCCTCATGCCAAACCAACTGACTTTGATTTCTTAAAGTTATTG
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAACCGGAACTGGATGGAAAATTTTATG
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAAGAGCAAAAACATATTATGG
CTGAACGTAATGTGCTCTTGAAAAATGTGAAACATCCGTTTTTGGTTGGATTGCATTATT
CCTTCCAAACAACTGAAAAGCTTTATTTTGTCTGGATTTTGTAAATGGAGGGGAGGGAC
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA
CCACATTTTGTGGGACACCAGAGTATCTTGACCTGAAGTAATTAGAAAACAGCCCTATG
ACAATACTGTAGATTGGTGGTGCCCTGGGGCTGTTCTGTATGAAATGCTGTATGGATTGC
CTCCTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG
ACAGGCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAATCATCCTTTTT
TTGAATCACTCAGCTGGGCTGACCTTGTACAAAAGAAGATTCCACCACCATTTAATCCTA
ATGTGGCTGGACCAGATGATATCAGAACTTTGACACAGCATTTACAGAAGAAACAGTTC
CATATTCTGTGTGTATCTTCTGACTATTCTATAGTGAATGCCAGTGTATTGGAGGCAG
ATGATGCATTGCTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTTGTGAGCAG
TTTGCCATTACAGAAACCATTGAGCAAAATAAGTCTATAGATGGGACTGAAACTTCTATTT
GTGTGAATATATTCAAATATGTATAACTAGTGCCTCATTTTTATATGTAATGATGAAAAC
TATGAAAAAATGTATTTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT
TGATTAAATTTATATTCTTGTTTAATAAGCTTATTTTAAACAATTTAAAAGCTATTAT
TCTTAGCATTAACCTATTTTTAAAGAAACCTTTTTTGCTATTGACTGTTTTTCCCTCTA
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTAAACAGTCAATTTCAAGTTCAGCT
AACATATATTAATACCTTTGTAACCTTTTGCTATGGCTTTTGTTATCACACCAAACTAT
GCAATTGGTACATGGTTGTTTAAAGAAGAAACCGTATTTTTCCATGATAAATCACTGTTG
AAATATTTGGTTCATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG
TTAACAATTGGAATAACTTTATTCTGCAGATCATTTAAGAAGTAACAGGCCGGCGGGT
GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCA

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FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCGCTCTCTACTAAAAATACAAAAT
TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA
ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG
CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22_R47805_H

ATGGCGCACAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA
CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT
GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGTGCTGCCACTG
CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCTCGACTCACAGAATGCTCAGGGC
TTCGAATGGCTCTTCTCGCTGGTGCCTGATAACTCCCCGTGCGGCTGAAGATGCTG
TACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCCACATCAAGGATGAG
CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGCTGGGTACCAGAAACACCTGTCGTCC
TGTGCGGCACCTGCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC
GAGGTGAAGACAGAGATCAGTGTGGAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTC
CCCCTGACGCTGAGGCCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC
ATCCAGATGAAGCTGACCTAGAGCGGGAAACCATTGAGCTGGTGCACACAGAGCCCACG
GATGTGGCCCAGCTGCCCTCCCGGTGCCCGAGATGCTGCCCGCTACCACTCTTCCTC
TACAAGCACACCCATGAGGGCGACCCCCTTGAGTCTGTAGTGTTCATCTACTCCATGCCG
GGGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTC
GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG
GCAGAGCTGACGGCAGAGTTCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG
CAGGCCTTCGCCAAGCCCAAGGGCCAGGGGGCAAGCGGGCCATAAGCGCCTCATCCGG
GGCCCGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23_H60215_H

CCACGCGTCCGGCGCCGCGAGCCATGGAGGGAGGCGGCGGCGGCGGCGGCGGCTCGGG
TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCCTCCAGCCCGGCCCCGGCCCCC
CGGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA
CCACCCGGCGAAGTGACACACCCAGAAGCTATGTCTTCGGCAGTAAAGTTTACAGC
ACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG
CACCAGGTCTGAATTCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT
GACCACAGACCCATTGAGGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA
TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTGGGCCA
GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTCA
TCCTTGGTCCCGCTCTGGGCAACTACCGGTGCCAAGCATAGTGCAGTGTGTCGCGAGGA
AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC
AAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTCAC
TGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTCCAGGACC
GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC
GCATCTGCCTCGTCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC
TCATCAACCTGCAGCACTACGTATCAAGGAGAAGAGGCTCAGCGAGAGGGGAGACTGTGG
TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCACA
GAGACCTGAAGCTGGGGAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCA
ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA
GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCGGCCGTACCGTGGCAAGCCCCAGT
ACATGTGGGCCCTGGGCGTGGTGTCTTCCACCATGCTGTATGGCCAGTTCCCCTTCTACG
ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGAGG
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGGACCCCC
AGCAGCGCCTGGCCGCCCGCCGACGTCTGGAGGCCCTCAGTGCCATCATTCATCATGGC

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FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCTTGACATTGATGACCAAATGA
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCCAGTACGAGTTTG
AGA ACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC
GGAGCTGGGTACCCAAGCGGCAGTTTCGGCAGCGCACCACCGGTGCGACGGCTGGGCCACG
ACGCACAGCCCATGACCTCCTTGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG
TGGCTGTCAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC
AGGGACAGGGACAGCCAGGTACACAGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT
TGGGATGATTGCTCGATTGTTTGGTTTTTAAATCTGAGAAGCCTAGATAACTAATCTGCT
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC
AAGAGGGAGGAGGGAGCCTGCTCACCCTACTCCAGGGCCTTCCCCAGCGGCCACCACTG
ACCTGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGCAGCTCGCTGCAGGCCCC
AGAGCGAGCTTCCCCTCCTCCCTGCTCTCCAGGCCCTGCCACAGCCTCTTCCGTCCC
TCTCTTTCTGATCCAGGCCCTCAGTCCAAGCTTTGGAAAACCTTACCTCATCTTAAAC
CAA ACTCAAATATATTTATTTTTTTTACCAT

SEQ ID NO: 24 SGK324_H

GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAGG
CCGCGGCCGGGGTCCGCGAGAGGGGCCCCAGCTCCTCCGGGGGCGAGCAGCAGCTCGGGC
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC
ACGCGGACCCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG
AACGGGGACCGCTACTTCAAGGGCCTGGTGTGTTGCCATCTCCAGCGACEGCTTCCGGTCC
TTCGATGCGCTCCTCATAGAGCTCACCCTGCTCCCTGTCCGACAACGTGAACCTGCCCCAG
GGTGTCCGCACTATCTACACCATCGACGGCAGCCGGAAGGTACCAGCCTGGACGAGCTG
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTTCGTAAAGTCGATTACACC
AAAAATATTAATCCAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT
GCTGCCTCCTCTGTGAAAAGTGAAGTAAAAGAAAGTAAAGATTTTCATCAAACCCAAAGTTA
GTGACTGTGATTGGAAGTGGAGTGAAGCCTAGAAAAGCCGTGCGGATCCTTCTGAATAAA
AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC
TCAGGAGTCGTCAAGAGGCTCTGCACCCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG
CATCTGCCAGACTTTTTTGGTGATGACGATGTTTTTATTGTCATGTGGACCAGAAAAATTT
CGTTATGCCCAAGATGACTTTTGTCTGGATCATAGTGAATGTCGTGTCTGAAGTCATCT
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC
CGTTGCATAAGTCCTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT
GAGAAATACAAAATTGGAAAGGTCAATTGGTGATGGCAATTTTGCAGTAGTCAAAGAGTGT
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT
ATCATTATGCTGGTCGAGGAGATGGAAACAGCAACTGAGCTCTTCTGGTGATGGAATTG
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTGACCAAGTACACTGAGAGAGAT
GGCAGTGCCATGGTGTACAACCTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG
TCTTTGAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAACTGGCTATGGCCTGAAG
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTCTGTGGATTCCCACCATTC
CGAAGTGAGAAACATCTCCAGGAAGATCTCTTCGACCAGATCTTGGCTGGGAAGCTGGAG
TTTCCGGCCCCCTACTGGGATAACATCACGACTCTGCCAAGGAATTAATCAGTCAAATG
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG
TCAGATGATGCCTCCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAACAG
CACTTTAATAATGCGCTCCCCAAACAGAACAGCACTACCACCGGGGTCTCCGTCTCATG

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FIGURE 2R

GTGAGTGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCTTCCGTAGTCCTATTTTCATATGA
AGATTGGCTTGGCATGTGGAGGGCACTCATTCCGGCAACTCCCAGGCTTTGGGCACTGTGT
GGAGGGGCTTGTGTAGGGACCAGCAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC
CTGGCTGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACCTCCCTGCCTACCCCAAGGCC
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA
AAGCTAAACATATTTTCAGTTTTAAAAAATCAGTGTTTTATAAAACACAGTTTGGGGCTTT
TAAAGGTACATAATCAAGGAAAAAATATATATTCAATTTTCAGGGTTGGTAACATTTTA
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT
TCTTAAGGCAACTCTCCTAAATACATAAACACAACAAATTAATGAAAAGTGACATGAG
AGTAAATGAATCAAAAGGAAAAAACATTGAACCAGAGGTGAGGGCAGCACACCCGCAGCA
GCTGTCCAGGCCTGAGCCAATGCAACCCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG
GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTTCGAATCA
GACCTGCCAAGGTGATGGGCGTCTGAGTTTTCACATCTGGGCCCCCGTGACCCCACTGAG
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCACTCGTACTTGGGACAGGCCT
CTCATCCTCTGGGAAGGTCTCTCCTTGTCTTCTACCCAACTAGAAGGGAAACAGTGGCATA
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA
GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCCACACTCC
CCACACCCCCACACCCCCACATCCCCACCATAATTACCCACCTCCAAATATCTCAT

SEQ ID NO: 25_W30246_M_SGK324_M

ACCAAGTCCTCCAGCTCCTCTCCAACCAGCCCGGAAGTTTCAGAGGATTGAAGATTTCT
GCTCAGGGCAGATCTTCTTCCAACGTAAACGGTGGGCCTGAACTTGACCGTTGCCTGAGC
CCTGAAGGTGTGAATGGAAACCGTGCTCCGAGTCGTCCCCCTTCTGGAGAAATACAGA
ATAGGGAAGGTCATCGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCGTGGACAGGTAC
ACTGGAAAAGAGTTTGCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAGGAGCAT
CTGATTGAGAACGAAGTGTCAATCCTGCGCCGAGTGAAGCACCCCAACATCATCATGTTG
GTTGAAGAGATGGAAACAGCAACTGACCTCTTCTAGTGATGGAAGTGGTCAAAGGTGGA
GATCTCTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCAGGCCA
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG
GCAGCTGGTGTGATTACATACTTCTCTGTGGATTCCCAACATTCCGGAGTGAGAAC
AATCTCCAGGAAGATCTCTTGACCAGATCTTGCTGGTGGTGAAGCTGGAATTCCAGCCCC
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTAGGAAATGCTTATGAAGCTGG
CCCGTGGGCTTCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG
TGTCATCTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC
CGCGGGGACGGGGGCATGGTGTCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC
TGGCAGTTTTTCCCTGTTTTCCACCACCCCACTCTTTTTTAATAATTGTATATACTGTACT
TGTTCTACTTGCTTGTCTTTAAACAGGGGCCCCACAGTTCACTCTCACTGTTAGATTT
TGCCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

SEQ ID NO: 26_AA383293_H

CCAGCAGCCAAGAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG
CTGGTGGTGAATCAACGCCGCTTCCCCACCATGGAGGCCTTCTCTGCGAGGTGACATCA
GCTGTGCAGGCCCCACTGGCTGTGCGTGCCCTCTACACACCTTGTGATGGCCACCCTGTC
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

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FIGURE 2S

CACAAGCTCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTTTCAGGAATGGGGACCTGGTA
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAACTGTGTTG
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG
GGGCTCCCACTGTGAGCAGGGAAGGAGCTGGTAAGTGGCCATTACTATGTGGCTGTGCGA
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA
GGCAATGAAGCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCCAAGCCTCTT
GGAAGGAAGGCTAAGAAGGAGACATGCCCTAATCGTGACCCTGACCCTGAAATACCAGCAG
TCAGAAACAAGCAGAGACGGGCAATCATTCCCATCAGGAGTTATAGGAGTATATGGAGCT
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGGAACAGGTTACTTGTCTGCAA
GACTTTTTTGGTGATGACGATGTTTTTATTGTCATGTGGACCAGAAAAATTTTCGTTATGCC
CAAGATGACTTTTGTCTGGATCATAGTCGTCGACGGCTCCTGAGAGAGCACCAGGCGGGC
TTTGAGAAGCTCCGACAGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA
TGATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG
GAGCCCAAGACGAGGCCAGAAGAGAACAAGCCAGAGCGGCCAGCGGTGGAAGCCACGG
CCCATGGGCATCATTGCCGCCAATGTGGAAAAGCATTATGAGACTGGCCGGGTGATTGGG
GATGGGAACCTTTGCTGTGCTGAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCG
ATGAAGATCATTGACAAGTCCAGACTCAAGGGCAAGGAGGACATGGTGGACAGTGAGATC
TTGATCATCCAGAGCCTCTCTCACCCCAACATCGTGAAATTGCATGAAGTCTACGAAACA
GACATGGAAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTTGACGCCATC
ATAGAAAGTGTGAAGTTCCCGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGGACCTCAAGCCGGAACCTT
TTGGTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTTGGACTTGCA
AAGCATGTGGTGAGACCTATATTTACTGTGTGTGGGACCCCAACTTACGTAGCTCCCGAA
ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGCGTGCTGGCGTGATCCTC
TATATCCTGCTGTGTGGCTTTCCCCCATTCGCGAGCCCTGAXXGAGGGGACCAGGACGAG
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTCTCTCCCCCTTACTGGGACAATATC
TCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTGGTGGTAGACCCCAAAAAGCGCTAC
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG
AAACGACAGAAGCAGGTGTCCCCCAGCAGCGATGGTCACTTCCGGAGCCAGCACAAAGAGG
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCCAGTTCTGCTC
AAGGACAGAGAAAAGGATAGAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTCACATA
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAAAAAATTAAGT
CAATGTTAAATGTCAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATACATTTT
TGGGGGGTAAGCATTGTCTCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC
CTTTGTAACCAAGTTTATTCTGTACTACAGGAGTGGTGCTTACCAGGGTCTAAACTCCCC
CTGTGAGATTAATAAGGTGCATTG

SEQ ID NO: 28_AA197883_M

ATGCCAACC CGCGCGGTCTGCGCCCGCGCCCGCCAGCGACCCCGCCCCGCGGCA
CCCAGTCGCCCTGCGCCTCCCATTCGCGGCCACCGAGGCCCATGTGACCATTCTCTGAAA
TGCTTAAGCTCGAAGATCTCTGAGAGAAAGCTGCCAGGCCCTGGTTACCTGCGGGACGA
GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGCCGTCATGCCGCTGTTTACGCCCT
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCACTGAAGCCCAGGGTGGTGACG
GTGGTGAAGCTGGGTGGGCAGCCCCCTCCGTAAGGCCACCCTGCTCCTCAACCGGCGCTCA
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG
AAGAACGACCGTGTGCGGAAGCTGTTACCCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT
GACTTCTTCCGGGAGGGTGATGCTTTTATAGCTATGGGCAAAGAGCCGCTGACATTGAAG
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCCCT
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCAGCAAGCTTCTGAAAGGA

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FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAGAAG
TGGGTAAGAGGGGAAACAGGAGTCAGAACCTGGTGGCCCGCTTCACCCGGGGCAGCCACT
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC
GGGGAGATTGTCAGATGTGAGAAGTGTAAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG
AGGGAGCCGTGCCCGCTGGGAACCAAGTGAGCTGGACCTGGGGAGAGCTCAGAAGAGGGAT
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
GGAGAGGAAGGGTGGAAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA
ATGAGGAGGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC
AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA
GAGGAGGGGGCCGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAAGCATGCC
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGAG
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGACAGTGAG
ATTTTAATCATCCAGAGTCTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTGATGCC
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCGAGGCTGCAGTTATGATCACAGACTTGTGT
AAGGCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC
CTCCTGGTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGCTCCT
GAAATTCCTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC
CTATACATCCTCTTGTGTGGCTTCCCCCTTTCCGAAGTCCTGAGAGGGACCAAGACGAG
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCCTCTCCTTACTGGGACAACATT
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC
ACGGCCGAACAGGTCCTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG
AACTCACAGAAGGAGGAGTCCCCCAACAGTTTAGGTCACTTCCAGAGTCAGCACAAAGAAG
GTTGCAGAGCAGATGCCATAA

SEQ ID NO: 29_DRAK2_H

CTCCGCTGCTGTGCGCCAGGAGTCACTTCACGAGAAGCCAGGTCACAACCGTCGGCCCTTG
TCTGGAAAAGTAAAAGTGGATCCTGCCACGTTCCGAGCTCCCTGGCGCCTCGCCCGGCTG
GAGCTAGAGAACTCGTCCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCCCTGGA
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCCGAGCGGTAAAAATAAGTGAATAAAGAAG
CAGACCTGGGAATCACCTAACATGTGAGGAGGAGATTTGATTGCCGAAGTATTTCAGGC
CTACTAACTACAACCTCAAAATCCAATAAAAAATGGAAAACCTTTAATAATTTCTATATA
CTTACATCTAAAGAGCTAGGGAGAGGAAAATTTGCTGTGGTTAGACAATGTATATCAAAA
TCTACTGGCCAAGAATATGCTGCAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT
ATTAATCTTCATGAGGTCTATGAAAATACAAGTGAATCATTGATATTGGAATATGCT
GCAGGTGGAGAAATTTTACGCCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT
GATGTTATCAGACTCATTAAACAAATACTTGAAGGAGTTTATTATCTACATCAGAATAAC
ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCCTCTCGGG
GACATTTAAATAGTAGATTTTGGAAATGTCTCGAAAAATAGGGCATGCGTGTGAACTTCGG
GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACTATGATCCCATTACC
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT
TATTCGGAAGAACTTTTTTCATCAGTTTCACAGCTGGCCACAGACTTTATTTCAGAGCCTT

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FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA
CAGCAGTGGGACTTTGAAAACCTTGTTTCACCCCTGAAGAACTTCCAGTTCCTCTCAAAC
CAGGATCATTCTGTAAGGTCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC
TGTGGTGATAGAGAAGACAAAGAGAATATCCCAGAGGATAGCAGCATGGTTTTCCAAAAGA
TTTCGTTTCGATGACTCATTACCCAAATCCCCATGAACCTTGTTTCAGATTGCTCTGTAG
CACTTTTTTCTTTGACTCATTGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACCTTTTCCATGGAATA
ATTTAGGGAAGTGTTTTAATGTTAAATTACTAGTTGCTAGCATGTTATGATTTTCATATCC
TGAGATAGCTCTGCAGATAAGAAAAATTTTAAATATATGACAAAAAGTAAATTGTACAT
GTGAAAG

SEQ ID NO: 30_W44160_M DRK2_M

CCAGACGCGGCTGCACCTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG
GTGCGCCGCCGGGAGTCGCCTCACAGGGGCTGGCTGACGGCGACCAGCCGTTGTGGGGAA
GAGTGCGAGGTAAAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA
GGAGATTGCGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCCAAAGAACTTGGGAGAGGAAAAT
TTGCTGTGGTTAGACAATGTATATCAAATCAACTGGACAAGAGTATGCTGCCAAATCCC
TGAAAAAGAGGAGAAGAGGGCAGGATTGCCGGGCGGAAATTTCTGCATGAGATAGCTGTGC
TGGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC
CTGAGTTAGCCGAAATGGTATCTGAAAATGATGTTATCAGACTCATTAAACAAATCCTTG
AAGGAGTTCATTATCTACATCAGAATAACATTGTTACCTTGATTTAAAGCCACAGAATA
TACTTTTGAGCAGTATATACCCACTCGGGGACATAAAAATTGTAGATTTTGGAAATGCTC
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC
CAGAAATCCTCAACTATGATCCCATACCACAGCAACAGATATGTGGAATATTGGCATAA
TAGCGTATATGTTGTTAACTCATACATCACCATTTGTAGGAGAAGATAATCAAGAAACAT
ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTTCATCAGTTTCAC
AGCTGGCCACAGACTTCATCCAGAGCCTTCTAGTAAAGAACCCAGAGAAAAGACCAACAG
CAGAAATCCTGCCTATCCCACTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTTCATC
CTGAGGAACTTCAGGCTCCTCTCAAATTCAGGATCTGACTCTCAGGTCTCTGAAGAGA
AGACCTCCAAGTCTCCTGTAATGGGAGCTGTGGAGCCCCGGGAGGACAAGGAGAACATCC
CTGAAGATGGCAGCTTAGTTTCTAAAAGATTTGATTTCGATGACTCCTTGCCAGCCCCC
ATGAACTTGTTCCAGATTTGTTCTGTGTAGCATTTTTCTCTGTGACTCATCTGGACTGACT
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT
TATAAATGCACCTTCTGCTTAGAAGAACTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG
GCTAGCATATCATTTCTTGCTGAAATGTTTTGCAGAGGAAAATATTTAAGTATATGA
CAAAAAATGTAAATTGTGTTTAAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA
GACTTATAAAATGGGTTATATTATGGTTAGTAAAGTTGAAAAAAATGAAAACAGGAAT
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAAATACTCCAGAGAGAGTTTA
TAGTTGAAAGTATTTCCAGTTACCAATAATAGCTTGAACTGTAAGATTTTCTTTGTGT
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGGTTGATCCAGGCTGTTTCTC
TGCAACCCGAGTCAAACTCGACATCATTTCCAGCTCATGTATTTTGTACGTGCATCATA
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAAATAAGAGGCCCTTTGTCTCTAGA
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTTGGATGTCTCCTAAGTCT
CAGGATAGAAGCCCATCATTAGAGCATAGGCACTTCAGGAATCTTGTGTGAAATCTTAG
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA
CACACACATGGGAGTGTTTCAGTGTTGTCCGTGGTCAATATCTATGTTTCAGTCTGATGG

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FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAGGTCTGTAATA
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA
ACAAATTAAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA
ATTGTTACTAAAATTCCAAATTCTTTAGATAACTTTAACTATTTAAATTGAGCATTGCT
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTTAAAGGAAAAGTTGT
TTGCCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT
GATAGATAAAATACAGCCTTTAAACAACCTTC

SEQ ID NO: 31_H01248_H, DRK1_H

ATGATCCCTTTGGAGAAGCCAGGCAGCGCGGCTCCTCCCCAGGCGCCACCTCAGGCTCG
GGCCGGGCAGGCCGGGGTCTGAGCGGGCCGTGCCGGCCGCCCGCCGCCAGGCCCGC
GGGCTGCTGACAGAGATACGCGCCGTGGTGCGCACCAGCCCTTCCAGGACGGCTACAGC
CTGTGCCCCGGGCGGGAGCTGGGCAGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAG
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAGAAGAAAAGGCCAAGAT
TGTCCGATGGAATAATTTCATGAGATTGCTGTACTTGAAGTACACAGACAATCCTTGG
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT
GCTGCTGGGGGTGAAATCTTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA
AAAGATGTTCAAAGACTTATGCGACAGATTTTGAAGGTGTTCACTTTTTACACACTCGT
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTG
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCCTAGTTATGATCCTATA
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTTAACATATGTCATGCTTACAGGAATA
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACA
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTTCAAGATGGAAAAGGCACTAGAAGAAGCA
AATGCCCTCCAAGAAGGTCATTCTGTGCCTGAAATTAATTCCGATACCGACAAATCAGAA
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA
TGCAGACAGTCTGAAAAAGAGAAAAATGGAGCAAAAGGCCATTTCCAAACGATTTAAATTT
GAGGAACCTTTGCTACAAGAAATTCAGGAGAATTTATCTACTGA

SEQ ID NO: 32_AA021445_H

CGGGGCTGCCGGGGCGGGACTGGGGGAGCCGGGCCCCGCGGGCCGCCTGCTGCCTCCGCC
CGCGCCGGGGTCCCCAGCCGCCCCCGCTGCCGTGTCCCCTGCGGCCGGCCAGCCCGCTCC
CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCCGTATCGGCTACTACGAGATCGACCG
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT
TTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCCATATCATCAGGCTCTACCA
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTCCGAAGTTCAA
ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTGCGAACATTTGTTTCATCGTGATTTAAA
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAATAGCAGATTTTGGTTTCAG
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCCAAAGTGGACATCTGGAGCCTTGG
AGTTGTCCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTGATGGAAGCACACTGCAGAA
TCTGCGGGCCCCGCTGCTGAGTGGAAGTTCCGCATCCCATTTTTTATGTCCACAGAATG
TGAGCATTGATCCGCCATATGTTGGTGTTAGATCCCAATAAGCGCCTCTCCATGGAGCA
GATCTGCAAGCACAAGTGGATGAAGCTAGGGGACGCCGATCCCACTTTGACAGGTTAAT
AGCTGAATGCCAACAATAAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCCT
CTTGGCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

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FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA
AACCCTGCGTCTCGGAGCACTTCCTAGCATGCCCCAGCCCTGGCCTTTCAAGCACCAGT
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT
GATCAACCCAGAGAACCAAATTGTGGAGCCGGATGGGACACTGAATTTGGACAGTGATGA
GGGTGAAGAGCCTTCCCTGAAGCATTGGTGCCTATTTGTCAATGAGGAGGCACACAGT
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT
TCCTGGAGTCAACCCCCAGGCTCCATTCTGCAGGTGGCCCCCTAATGTGAACTTCATGCA
CAACCTGTTGCCTATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC
TCTCCTACAGCCGCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC
ATCAGATGGAGGAGCCAACATCCAATGCATGCCAGCAGCTGCTGAAGCGCCACGGGG
ACCCTCTCCGCTTGTACCATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA
GAGCTCAGACGGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA
AAGACATACTGGCCATGACCAACCTACAGCTGAGATCCCACCGACCTACAACGGCA
GCTAGGACAGCAGCCTTCCGTTCCCGGTCTGGCCTCTCACCTGGTACCTGATCAGCA
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCTGT
GCGCCGTTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAT
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA
CGGGGGGAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCTCTCTCA
GCCATCTCCACCTCTTCAGGCTGCATGTGAAATCAGCCAGCCCTCCTTACCCATCAGCT
CCAGAGGTTAAGGATTCAGCCTTCAAGCCACCCCCCAACCACCCCAACAACCATCTCTT
CAGGCAGCCCAGTAATAGTCTCTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC
TGCACTCTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC
TGAGAACTGTTTCTCTCTCTCCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC
TCAGTCACAGCAGGTCAACATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT
GCAGATGCAGCACCGTACCAACCTGATGGCCACCTCAGCTATGGGCACCGTCCCTTGTCT
CAAGCAGCTGAGTGCTGACAGTGCAGAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTCGGACCAGTCCCGGGGTTCT
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCCAAGCCCTGAAAGT
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGCACATCAGCAGCCGCCACACTA
TACCACGTCCGCACTACAGCAGGCCCTGCTGTCTCCACGCGCCAGACTATACAAGACA
CCAGCAGGTACCCACATCCTTCAAGGACTGCTTTCTCCCCGGCATTGCTCACCAGGCCA
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGCACAGCTCATTAAAAGGCAGCAGCAACA
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAAGTGTTCAGGCACAT
GAACCAAGGGGATGCGGGGAGTCTGGCTCCAGCCTTGGGGGACAGAGCATGACAGAGCG
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT
GCTACAAATCAGGGCACAAGAATGTGTCTCACAGGCTTCCTCACCCACCCCGCCCCAGG
GTATGCTCACCAGCCGGCACTGATGCATTAGAGAGCATGGAGGAGGACTGCTCGTGTGA
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAGGTTGCCA
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCCTGAATCTTTGCTAGGAAC
TGTGAGTCATGCCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAAGTCTGTCATT
CAGTAAAAATAAGGTGCCAGCAGAGAGCCTGTCATAGGGAACTGCATGGATAGAAGTTC
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCTC
CGTCCATGAGCACACAGGCCCCCGGCCCTCCAGAGACACCACAGATCCAGAACAGCGA
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT
TAGCTCTGCCCGGATGTCCGATGTCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTCATGAGCACCCAGA
CCTGAGTGATGGCAGCCAGCATTTAAACTCCTCTTGCTATCCATCTACGTGTATTACAGA
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTCAGCATGGAGCAGGCAGGCGTGTA

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FIGURE 2X

ACAAGAAACAGAGAGTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC
TGCTTTCCTCACATTGTTGTTTCATCCGTGTGCTGTTCTTTGGGTTCTGAGAGGGTTTGC
CATGTTTGCTTGTATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC
C

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CTGGGCCGCTGCCGGTCAGGTCGGCCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA
GGCGGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG
AACCAGCCAAATTTTCGAGACAGCTCAGCGCTTAGAGGAAGGTTTCATCTAAATAAAGGCC
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAAGAAGGCT
TATTTGCAAGTTTCTTCTTCTTCTGGGGTCCAGATTATTAGGTTCTCCAGCGCCCTGCAGCT
TGACAGAAAGAGAAGCATGAAATGAAGGTCAGAGATGAGATCCCGCAGCAGGGAGCTGGG
GGCCTCCAGGGGCATTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG
CAAACAGAAGCCTTTGTCTGGGGCACAGCCACCTACCACAAAGCATCAGACTCCACGTC
TGGCCAGAAAGTTCTGGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCTCTCACTAAA
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAATCCTTTTGAACCCTGGGCACCTGCTGT
CCTCAGTTGGCATCTCCACCCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG
CTGAGATGGAGACGTGAGCCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTCAG
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA
CTGACACAGGACATGTCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG
ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAACCTTCTCCAAGTGAAGCTT
GGGATTCACTCCCTAACCAAGAAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA
GACCAGAAAACCCAGAGGCTACTATCCCGAGAAATCTCCAGCATGGAAAAGCTGCACCAT
CCCAACATCATCCGCCTTTACGAAGTGGTGGAGACCCTATCCAAGCTGCACCTGGTGATG
GAGTATGCAGGGGGTGGGGAGCTCTTCGGAATAATTAGCACTGAGGGGAAGCTCTCTGAA
CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC
CAAATTATTATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG
AAGGTGGGCGATTTTGGATTGAGCACAGTAAGCAAAAAAGGTGAAATGCTGAACACTTTC
TGTGGGTCTCCTCCCTACGCTGCGCCTGAACCTTCCGGGACGAGCACTACATCGGCATT
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGACTGGCACCATGCCA
TTTCGGGCAGAAACCGTGGCCAAACTAAAAAAGAGCATCCTCGAGGGGCACATACAGTGTA
CCGCCGCACGTGTCAGAGCCCTGCCACCGACTCATCCGAGGAGTCCTTCAGCAGATCCCC
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC
CCTACACCTTTGGAACCTTTCCAACCTGGATCCCAAACATTTGTCGGAAACCAGCACTCTC
AAGGAAGAAGAAAATGAGGTCAAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT
ATTGAAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCAGTCATGATGCTACCAGAC
CCTAAAGAAAGAGACCTCAAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC
AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACCTAACCAAGATGATTGTT
GCTGCTTCTAAATTTTTTTTCAAGGACAACTTGAGTGAGAGACATTTTTTGTAAATTTTAAAT
AAACTTAAATTTGAGATATGCAAAAAA

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ATGTCCACTAGGACCCCATTTGCCAACGGTGAATGAACGAGACACTGAAAACCAACAGTCA
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

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FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAACTACAGACTGTTGAAA
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAAATTGGCAAGACATATCCTTACAGGCAGA
GAGGTTGCAATAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTGCAA
GTCATTGAAACTGAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA
TTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAAATAGCAGATTTTCGGTTTTAGC
AATGAATTTACTGTTGGCGGTAACTCGACACGTTTTTGTGGCAGTCCTCCATACGCAGCA
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAAGTGGATGTGTGGAGTCTGGGG
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCTTCTACATGTCTACAGACTGT
GAAAACCTTCTCAAACGTTTCTGGTGCTAAATCCAATTAAACCGCGCACTCTAGAGCAA
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTGT
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA
TATTTGTTATTGGGGAGAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC
AATCTTTCACCTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT
CCTCACCACAAAGTGACAGAGAAGTGTTCCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC
CATGCTGGACCAGCTATTCCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTCCCGGAAATCAAGTGGCAGTGCTGTT
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG
GCGGATATTCCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT
GGAATGACACGACGAAATACTTATGTTTGCACTGAGAGAACTACAGCTGATAGACACTCA
GTGATTGAGAATGGCAAAGAAAACAGCACTATTCCTGATCAGAGAACTCCAGTTGCTTCA
ACACACAGTATCAGTAGTGACGCCACCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC
AGTCGTAGCACTTTCACGGCCAGCCCCGGGAACGGCGAACCAGCAACATATAATGGCCCT
CCTGCCTCTCCAGCCTGTCCCATGAAGCCACACCATTGTCCAGACTCGAAGCCGAGGC
TCCACTAATCTCTTTAGTAAATTAACCTCAAACTCACAAAGGAGTCGCAATGTATCTGCT
GAGCAAAAAGATGAAAACAAAGAAGCAAAGCCTCGATCCCTACGCTTACCTGGAGCATG
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAATCCGCAAAGTGTTGGAC
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT
GGGCACGCGGAGAACCTCGTGCAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT
CTGAACGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

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AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCGTTGCCGGAACCTCTATCGCTTCC
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTGCTATTAAAG
ATCATTGATAAGACCCAGCTGAACCCCACTAGCTTGCAAGCTGTTTCAAGAGAAGTCCGA
ATTATGAAGGACTCAACCACCCCAACATCGTGAAGCTTTTTGAGGTGATAGAGACGGAG
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTGTTGACTACCTCGTG
TCGCACGGCCCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTACGCC
GTGCACTACTGTATCAGAAGAACATTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCGGCTTACAGCAATGAGTTACGCTG
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATACGCCGCCCCAGAGCTGTTCCAG
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCATCCTGTACACG
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC
CTCAGAGGAAAGTACCGGGTCCCCTTCTACATGTCTACAGACTGCGAGAGCATTCTGCGG

FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG
CGGATGCCGGGTGCGAAAGCGAGCTGCAGTGCAGTGGGCAGTGGAAGTCGAGGCTTGCCC
CCCTCCAGCCCCATGGTCAGCAGTGGCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG
CGGAAGGACAGCACTAGCACCCCTAACAACTCCCCCCCAGCATGATGACCCGAAGAAAC
ACCTATGTGTGCACAGAGCGACCAGGATCTGAACGCCCCGTCTTGTGTGCCAAATGGCAAA
GAAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCCTGGCT
CCCCCGTCAGGCGAGCGGAGCCGCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA
CCCCCAGCCTCACCCACGCTTGCCACGAGGCCGACCCCTGCCCTCCGGGCGGCTCGC
CCCACCACCAACCTCTTCACCAAGCTGACCTCCAACTGACCCGAAGGGTCACAGACGAA
CCTGAGAGAATCGGGGGACCTGAGGTACAAGTTGCCATCTACCTTGGGATAAAACGGAA
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

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GTAGCCGGCTTGGCGTGACCGTCGCCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT
GGCCTCCCTTCTTCCCATGGAGGTGCGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG
CCTTTCCAGAGCCTCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC
TGAGCCAGCAGGTGCTTTTCTCAGCCACAGACACCTGAGCAGAAGGAATGGGCTTTC
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC
ATCACTGGCTGCCCAGAATATTTGTACAAGTAACTGCACTGCCCTGCTGCCCTTGAGCA
CACGGACCCGTCCGAACCGCGGGCAGTGTGTCTGCTGCTCCCTGCTGCGGGGACTGTC
CTCAGGGTGGTCTCACCCTCTGCTTCCGGCCCCCTGTGTGCAACCCTAACAAAGGCCATCTT
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTGAGA
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT
GGTGTGTTGGCACGGTGGTGGACATCATCACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCTATGCTGCGTGGTGGTCTTGAGCCCCGT
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTCATGTGACAG
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC
AGACCTGATCCCTTCTGTGCAGTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA
GATTCAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGCCCCCTGTGAGCGGCTA
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCTCCTGCCGGATGG
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAGACGGA
GCTCCTGGGCAAGAATATCACTTTCTGATTCTGTTTCTACAGCTACATGGACCTTGC
GTACAACAGCTCATTACAGCTCCCAGACCTGGCCAGCTGCCTGGACGTGGCAATGAGAG
TGGGTGTGGGGAGAGAACCTTGGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA
GGATCCAAGGATTAATGTCGTGCTTGTGTTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG
GAAGCTGATGGAAAGCCAAGACATCTTCACCGGGACTCAGACTGAGCTGATTGCTGGAGG
CCAGCTCCTTTCTGCCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCCAGAAGG
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC
TGAACAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC
TGAGGATGGGGGCAGTGTGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG
GATGGGAGTCAGTGGTCCCAGCGGTTACAGCCTTGGGCTGGGGCTGCCCTGGGCCAAGCC
CCAGGCCAAGGGTCAGCTGGCGGGGGGCAGCCTCCTGATGCACTGCCCTTGCTATGGGAG
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCCTCTGGGATGGCAGG
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAAAACGACCGAGA

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FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGCAGGAGCCCT
GGATGTCCCCACGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG
CTATGCCTTGGCCACGGACCTCCCTGGGGCCTGGAAGCAGTGGAGGCCCAGGAGGTTGA
TGTGAATTCTGTTTCTGGAACCTCAAGGAACTCTTTTTCAGTGACCAGACAGACCAAAC
GTCATCAAATTGTTTCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCCTTGGCAGT
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCTGTGTCTCTGGATGACAG
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCCGGGA
GAGCTGTGTGGGACATGATCCAACAGAACCCTTGAAGTTTGTGTTGGTGTCTCTGAGCA
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTTCTTCCACGTTGGATGCTGGCCC
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTCACCTCCACGCC
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGGTGCCTACTC
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAAGACCTCCTCCACAG
CCAACCGGACTCAGCCGCCAGGACCCGCTGTTTCTTGGCAGCCTGCCCGGCTCCACCCA
CTCTACCGCTGCTGAGCTACCCGACCCAGCCTGGTGGAAGTGCTCAGAGCCAGACCCTG
GTTTGAGGAGCCCCCAAGGCTGTGGAACCTGGAGGGGTTGGCGGCTGTGAGGGCGAGTA
CTCCCAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC
TGCTGTGGACAAGGGAAAAACAAGGAGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT
CTTGAGGATTGTTGGATTGAGGATCCCAAACCTTGGGAAAGTTACTTTAGAGATCGCAAT
TCTATCCAGGTTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA
CCGCCACCCCAGGCTGGATGAGCCCTGCGGAGCTACATCTTCCGACAAGTGAGAGCAGG
CCAGAGCCGCTCTAGTGTGACAGTGGGATACCTGCGCTTGAAGGACATCATCCACCGTGA
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG
CTCGGCCGCTACTTGGAAAGGGGAAAATTATTTTATACTTTTTGTGGGACCATCGAGTA
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCCTTCTGTGAGCTGGAGGA
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCAAAGAACTCATGAGCCTTGT
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA
CCCGTGGGTAAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT
GAGTGATGTGGCCCAGGCTCAGGAGCTTTGTGGGGGCCCCGTTCAGGCGAGGCTCCTAA
TGGCCAAGGCTGTTTGATCCCGGGGATCCCGCTCTGCTGACCAGCTAAACACCAATTC
TTCTGCTTTTCTCCACTTGGTTTGGAAAATCACACAGTTTTCAGGCTCCATCTGTTTG

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CCACGCTCCGCATCCCTGCTTGGATGAGCCCTGGCGAGTTTCATCTTTTCGACAACTAG
TGTCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA
ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT
TAGAGAGGGGCAAACATATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG
TTCTCATTTGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTACCC
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG
TTATTTCATCCCCATTCTGCTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC
AGCCTTGCCCTGAGCAGCGGACCACTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA
GTGGCCTGCTGTGAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCAGGGAGACTCGTGGTGACCAGCACTGCT
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG
GGCAGTTGTATGGATTTTCAGGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

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FIGURE 2BB

TGACTTCTGCTTCTAGATTCCCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTTTATAACCTTGAAAATCATTCTAATG
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG
TGTTTTAAGTTCTCTATTTTTTGTGTTTGTGTTTTGCTTGTAAGTTTTTGAGACAGGATCTC
ACCATGTAACTTTGGCTGGCCTGGAACCTCAACTATGTAGACCAGGTAGACCTTAAACTGA
CAGATCTGCCTGCGCTTGCTCCCAAGCATTAGGACTGATGGTGTGTGTCAACCATGCCCA
GTTCTTCCTGGTTTTGTGTGTAGGTTTCTTTCCCACTGACTTGGTACATGTGACATGTGA
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAAATGGCCAGAATATTTATTTATTTT
CTTAAAAATTTTCCAAATTAAAGCTACTTAGTTAACAGTTAAACTGGCCAGGACTATATG
AGATAAACTTGGTTTTCTATTTCTTTTTGT

SEQ ID NO: 38_AA785735_H

GGCACGAGGCGCGCTGGCTGGGCCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA
GCAAGCGGAGCGCAGTTCCGCCAAGCCAAGCCGCGCTGCCAACCTCCCGCCCCGCCGCG
CTCCTGTCCGCCGTGTCTAGCAGCGGGGCCAGCATGGTCATGGCGGATGGCCCCGAGGCA
CTTGACGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACCTTATCAGGTAATGGAGACCAA
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAATTTTTGACTATCTTGC
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATCTGGCAAATCCTGTCTGC
TGTTGATTATTGTCTATGGTCCGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT
GCTGGATAACAACATGAATATCAAAATAGCAGATTTCCGGTTTTGGAAATTTCTTTAAAAG
TGGTGAACCTGCTGGCAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT
TCTGGAAGGAAGATTCCGGATTCCGTATTTTCATGTGAGAAGATTGCGAGCACCTTATCCG
AAGGATGTTGGTCTAGACCCATCCAAACGGCTAACCATAGCCCCAAATCAAGGAGCATAA
ATGGATGCTCATAGAAGTTCCCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA
TGAGCCATCCATCGGGGAGTTTAAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAA
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAAAGAGCTATAACCACTTGTGCCAT
TTATTTCTTGTGTTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGAGCAGAG
ACTTGATGGCCGCCAGCGTCGGCCTAGCACCATTTGCTGAGCAAACAGTTGCCAAGGCACA
GACTGTGGGGCTCCCACTGACCATGCATTACCGAACATGAGGCTGCTGCGATCTGCCCT
CCTCCCCCAGGCATCCAACGTGGAGGCCTTTTCATTTCCAGCATCTGGCTGTGAGGCGGA
AGCTGCATTATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA
CCCTGTGCCTCCTGTCTGTTGGTGCAGGAGGATGCCAGTCACTGCCAGCAACATGATGGA
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCCGAGGAAGACCCCGCTCATGC
CTTTGAGGCATTTAGTCCACACGCGAGCGGCAGAGACGGCACACTCTGTGAGAAGTGAC
CAATCAACTGGTCGTGATGCCTGGGGCAGGGAAAAATTTCTCCATGAATGACAGCCCCTC
CCTTGACAGTGTGACTCTGAGTATGATATGGGGTCTGTTTCAGAGGGACCTGAACTTTCT
GGAAGACAACCCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCAGAA
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGAGAGCATCAGATAC
CTCCCTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAGAACCAA
AGGAATTCTAGAGTTGAACAAAGTGCAGTTGTTGTATGAACAAATAGGACCGGAGGCAGA
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGATCCCCAGCT
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCAGCCT
TCTGTCAAAGGCCCAGAACACCTGTGAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

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FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA
ACTGCAGGCCCTATTTTAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA
GCAGCTGCCCCCTTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTTCA
CCTGACCCAGCCCCCTGAGCCCCGTCTGGAGCCTTCTCCGAGCAGATGCAATACAGCCC
TTTCTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCCTGCCCTCCACTTCCGGTCCCCG
GGCTGCTCCTCCTCTGCCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG
TGAGCTGCCAAGCGCTGCTTCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCAGAAGCCCAGGACTGCA
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCTGGTGAATTAGTCTCA
GCACAGGAATTGAGGTGGGTGAGGTGAAGGAAGAGTGTATGTTCTATTTTTATTCCAGC
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCTCCTGGTTCTGCCCCACCA
CAAAGTTTTCTGTGGCAAGTGCTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG
AACCCGGGAGGCGGAGCTTGCACTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCG
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGGCAG
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA
TTTTTGTCTTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC
ACTGGGGCACAGATAGAGAACCAGGCGGCAGCAGTGCTCGCAGACCCACCCAGGGAGAGC
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT
TTGTACATTAGTTTTACCAAGCACTTTCTCTTCTAACCCCTCACAACAATTCTATGAAATT
AGCTGGGGAGATACTGTCTTATTTTTTACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTGAC
TGGCTTCTGGTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTCCCTTCT
CTTTCCTCAGTAGCATCTGACTCTTTTCTAAGCAAACAGCTGTATAAAACAAAGCCCCCA
TTTTTGGTCAAGCACAGGGTGAATGTGATATTGTTCCCAACCTTATTCTCCACTCAACA
GCCGCTGGCTTTGGGGAAGAGGCCGCTTCCAGGTGACAGTGCAGCTGTCCAGGTGGCCG
TGCACTGAACCAGGCTGAGGGAGACAAAACCCCGCAGACCCGCTGCCCTTTCAGCGTCC
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC
AGCAGTTTTCTACAGAACACCCCCCTTCTCAATTGCCAAGGGGCCGATCGCACGGCATC
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCATGAACCTCAGCCTTGT
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGCCCCATCAACTAGAAGTGCTTATTA
CTTTTAGGATTAAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTTCAGAGGCA
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT
ATGACCCCAAGATGGAATAATGTCACATTCCCCAGTGCAGATAATGGGCTGCTGGCTC
TGTGGTGTCTGTCTGCAGAAGATTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC
CACCATGGGTGGTAAGAGAAACCTGCCTTCACCAAATCTCTGAAGGGGAAGAAGTGA
GAGAAAGGTTTGCTTCACTTCGGGGACTGCAGTTTGAGAAATAAAAGGGATACAGAGATA
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT
TTTCTGTGTGCTTTTTTTTAAATTACTAAGAAAAAATTGGTGAGTTTCACTAGCTTTGGTA
TTATGAGTGCAAATCATAATAGCTCCAATGTGAAAAAATAATCAAAAGTATAACTTGT
ACTTAATGTTAGAAAATTGCCTAAAAATGCAGTGTAAATAAATCTCTGTACCAAATAGT
AATTTAAATGGGGTAATTTTCTGCAAGGAAAATGTACTGTTTTTATGTTTCCAACCTCT
TGA

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FIGURE 2DD

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GCTGTGGCTCCCCGTCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTTC
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGAGAGCTAGCCCGGCCGCTGGCGGAAGGG
CTGATCAAGTCGCCCCAAGCCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG
CACAACCTGCGGCACCGCTACGAGTTCTTGAGACCTGGGCAAAGGCACCTACGGGAAG
GTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCA
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTG
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC
TACCGGGAGCCACCTAAACCCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG
GTGAACCCACCCGCCGGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT
GACTCTGCCCCGCGCTCCATGGCTGACTGGCTCCGGCGTTCTTCCCGCCCCCTCTGGAG
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC
CCTGGCCTGGAGCGCCAGCATTGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCAG
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTCAGCCTCTGCAGAAGGGGTACAGGAGGAC
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCCAGGGCAGGCTGCCCCCTGCTCCCCAAG
AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCC
AGTGAATCTGGGGAGCTCTTGACGCGAGCGGACGTGTTTGTGAGTGGGGATCCCAAGGAG
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT
GGCAAGTTCTCCAGACAGCCTTGGAGCTCGCGGGCCCCACCACCTTCGGCTCCCTGGAT
GAACTCGCCCCACCTCGCCCCCTGGCCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG
GACAGCATCCTGTCTCTGAGTCCTTTGACCAGCTGGACTTGCTGAACGGCTCCAGAG
CCCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCTCA
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTT
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGTCTCA
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCCGGTGAGGCTCTCAGATGCAGCTGG
TTGCACCCCGAGGGGAGATGCCTTCTCCCCACCTCCCAGGACCTGCATCCCAGCTCAGA
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG
AAATGCGCCAAGGGTTTCAGTGTCTGTCTTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA
GAGGGGAACGGGAATGCCCGGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG
GGCCACAGAGA

SEQ ID NO: 40_AA426580_H, MAK_V_H

ATGCCGGCGGCGGCGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCCTGGGGGCGGCGGC
GGCGCGGAGGACGCGGCCAGGCCCCGCGCGGCCTGCGAGGGAAGTTTCTGCTGCTGCTGG
GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCAGCACCACAAGCGCGTGGGCAAC
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGACCAAAAAG
GACACCTATGTCACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC
CCCAATATCACTCAGCTCCTTGATATTTAGAAACGGAAAACAGCTACTACCTGGTCATG
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

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FIGURE 2EE

TCCGAAGCCCGCAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC
AAGCTGATTGACTTTGGTTTGAGCAACTGCGCAGGGATCCTGGGTACTCGGATCCGTTT
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG
CTGCCTTTTACGGTGGAGCCTTTTCAAGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA
GAAATGAACCCCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTTGCCTCTCTC
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTGAGCAGGCACTGGCGAATCGCTGGCTT
AATGAGAATTACACGGGCAAAGTGCCCTGTAATGTCACCTATCCCAACAGGATTTCTCTG
GAAGATCTGAGCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC
GACGTGATCAACACTGTGCTCTCCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTC
TTAAACAAGAACTGGAGCGCTATTTGTGAGGAAATCTGACATCCAGGACAGCCTCTGC
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCTTATGAGGCC
TCTCTGGACACCTGGACACGAGATCTTGAATTCATGCCGTGCAGGATAAAAAGCCCCAA
GAACAAGAAAAAAGAGGGGATTTTCTTCATCGACCATTCTCCAAGAAGTTGGACAAGAAC
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTGAGAACACCAAGCC
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCTTTGGCTGC
CGCAATATTTTCCGCAAACCTCAGATTCCAATTGTGTGGCTTCTTCTCCATGGAGTTC
ATCCCCGTGCCACCGCCAGGACCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA
GGGCCCCGAAGCACTGGCATCCCCACAAGGAAGACCCCTGATGCTGGACATGGTGC GC
TCCTTCGAGTCTGTGGATCGCGACGACCAGTAGAAGTGCTGTCTCCCTCTCATCACTAC
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCAGCGAGAGGACGCTGTCC
CCGGGTCTGCCATCCGGAAGCATGTGCGCTCTCCATACTCCTTTGCATCCAACCTCTGGTC
TCTTTTGCTCACGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT
CCGGTTCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCCACTGCAGCCCCCTAGCCCCGTG
AACCTTGCCCTTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

SEQ ID NO: 41_Z36720_H

ATGGACACAAAGCTGAACATGCTGAACGAGAAGGTGGACCAGCTCCTGCACTTCCAAGAA
GATGTACAGAGAAGTTGCAGAGCATGTGCCGAGACATGGGCCACCTGGAGCGGGCCTG
CACAGGCTGGAGGCCTCCCGGGCACCGGGCCCGGGCGGGGCTGATGGGGTTCCCCACATT
GACACCCAGGCTGGGTGGCCCCGAGGTCTTGAGCTGGTGAGGGCCATGCAGCAGGATGCG
GCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAAGATGGTGGCTGCGGTGGACAGGGCC
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTTCATGCAGGGG
CGTGTGCCCTGGAGGAGAGGCAGCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG
AAGGATAAGGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG
ATCATGGTGACAGCGGCAAATAAAGAGCGAGTGGAAGAAGAGGGAGGAAAACCAAGCAT
GTGCTGAGCACCACTGGGGTGCAGTCTGATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA
GCTGACCCCGCCAGGCAGTGGTCTCACCGGGCCAGGGAGATGGTGTCTTCTGGCCAGCC
CAGGCATTCCCTGGCCACCTGCCCCCTGCCACAAAGGTGGAAGCCAAGGCTCCTGAGACA
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG
GTCTCCCCGAGCCTGGAGGTTGCACAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT
GACCTTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA
GGGCCTCCAGGGCTGCCAGCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGT
CTTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGAGCCTTGGACCCACCCTCACCACAGAGGCTCCA
GCAGCTGCCCAGCCAGGCAAGCAGGGCCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCT
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCCGCTGCAGGAG
AGCAGCAGCCCCGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG
CAGCAGGGCAAAGCCCAGGGGCGGGAAACCCTGAGCCTGAGCAGGACTGTGCAGCCAGG
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCAGGCGCCGAGGCTGGCAGCGTG
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTCGG
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCTTCGAGAGCAAGCACAGCTGC
ACCCTTGTCATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG
TACCACCTGACTGAGCTGGATGTGGTCCTGTTTACCAGGCAGATCTGTGAGGGTGTGCAT
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT
CGAGAGAAGCTGAAGGTGAACCTCGGCACTCCTGAGTTCCTGGCCCCAGAAGTCGTCAAT
TATGAGTTTGTCTCATTTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTCAATTGTA
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC
TTTGTTCCTCCGTTGCTGGTCAAAGAGAAGAGCTGCAGAATGAGTGCCACACAGTGCCTG
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAA
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACCTTCTCCCTAA

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GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCCACTGACGTGGAGGTGGATTGG
CTGTGCCGTGGCCGCTGCTGCAGCCTGCACTGCTCAAATGCAAGATGCATTTTCGATGGC
CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGCTTACACCTGC
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCGGCTGACCGTGCGGCCCTCG
TTGGACCCCTGTTTCAACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC
TGCCCCATGGAGGAGAGTGAGAACTTGCGGCTGCGGCAGGACGGGGGTCTGCACTCACTG
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTGAGTGTGTTAACACC
CATGGCCAGGCCCCACTGCTCAGCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCCTCA
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG
CTGGAGCGGCTGTCCATTCCCGACTTCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCCAACCATCAGCTGG
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT
GTCCATCGCTTGGTGTTCCTGCCGTGGGGCCTCAGCACGCCGGTGTCTACAAGAGCGTC
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCACCTGTATGTACAGATGTGGTC
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGAATCCCTGACGTACACA
GTGCAGCACCAAGGTGCTGGGCTCGGACCAAGTGGACCGCACTGGTTCACAGGCCTGCGGGAG
CCAGGTTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCTCTCAGC
ACCATGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGGAG
CACGGCCCCAACCTGGAGGAGGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG
GTGGAGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGCCAGGTGCTC
TGGAGGAGCTGCCAGGGGCCCTCCTAGAGGCACGGGCGGTGTGTACGAGCTGAGCCAG
CCAGATGATGACCAGTACTGTCTTCGGATCTGCCGGGTGAGCCGCCGGGACATGGGGGCC

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FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTCACGGCACACAGACCTGCTCGGTACATTGGAGCTG
GCAGAGGCCCTCGGTTTGGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAACT
GCTCGCTTTCGGTGGTGGTTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC
CTGGTGGTGTCTCAGCACGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCAGAAC
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTACAGCTCAGACAGCTATG
GAGGTTCGAGGGGGTTCGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCTACTTGCGGCGCATAGTGAGCGT
AGCTCCGGCCTGGAGTTTTCGGCCAAGTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA
GCGCGTCGGGAGGCCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT
GAGGCCTTCGAGAGGCGCCGGGACTGGTCATTGTACCGAGCTCTGCACAGAGGAGCTG
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG
CAGGTGCTAGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG
CCTGAGAACCTGCTGGTGTGGGATGGTGTCTGCGGGCGAGCAGCAGGTGCGGATCTGTGAC
TTTGGGAATGCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT
GAGTTTGTAGACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG
CCTGTGGGTGTTGTTGCCTTCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAAT
GACCGGACAACATTGATGAACATCCGAACTACAACGTGGCCTTCGAGGAGACCACATTC
CTGAGCCTGAGCAGGGAGGCCCCGGGGCTTCTCATCAAAGTGTTGGTGCAGGACCGGCTG
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTTCAAACTCAGGCAAAGGGCGCA
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCCCCGGCGAGGTGGCAGCGCTCCCAG
ATCAGCTACAAATGCCACCTGGTGTGCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCCA
GAGCGGGTGTGGGTGACCATGCCCAGAAGGCCACCCCCCAGTGGGGGGCTCTCATCTCC
TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCCCACTGCAGCCC
GAGTTCTCTGGCTCCCCGGGTGTCCCTCACAGACATTCCCACTGAGGATGAGGCCCTGGGG
ACCCAGAGACTGGGGCTGCCACCCCCATGGACTGGCAGGAGCAGGGAAGGGCTCCCTCT
CAGGACCAGGAGGCTCCCAGCCCAGAGGCCCTCCCCCTCCCCAGGCCAGGAGCCCGCAGCT
GGGGCTAGCCCCAGGCGGGGAGAGCTCCGCAGGGGCAGCTCGGCTGAGAGCGCCCTGCCC
CGGGCCGGGCGCGGGAGCTGGGCGGGGGCTGCACAAGGCGGCGTCTGTGGAGCTGCCG
CAGCGCCGGAGCCCCGGCCCCGGGAGCCACCCGCCTGGCCCCGGGGAGGCCTGGGTGAGGGC
GAGTATGCCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGAGGCCCCGAGGAT
GGCAAGGTGAGCGGCCTCAGGGGTCCCCTGCTGGAGAGCCTGGGGGGCCGTGCTCGGGAC
CCCCGGATGGCACGAGCTGCCTCCAGCGAGGCAGCGCCCCACCACCAGCCCCCACTCGAG
AACCAGGGGCTGCAAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG
CACCGCCGAGCGGGGGCGCCCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCCGTAGGCTA
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCCAGCCATCCAGCCCTGCACGGCCC
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT
GCTCCGAGCCCCCGCACCCAGCCTGCCCAAGACAAGGCTCCAGAGCCCAGGCCAGAA
CCAGTCCGAGCCTCCAAGCTGCACCACCCCCCAGGCCCTGCAAAACCTTAGCGCTGCC
CTCACACCCTATGCTCAGATCATTAGTCCCTCCAGCTGTACAGGCCACGCCAGGGCCCC
TCGCAGGGCCCTGCCGCGCCGCTTCAGAGCCCCAAGCCCCACGCTGCTGTCTTTGCCAGG
GTGGCCTCCCCACCTCCGGGAGCCCCCGAGAAGCGCGTGGCCCTCAGCCGGGGTCCCCCG
GTGCTAGCCGAGAAAGCCCCGAGTTCCACGGTGCCCCCAGGCCAGGCAGTCTCAGT
AGCAGCATCGAAAACCTGGAGTCGGAGGCGGTGTTTCGAGGCCAAGTTCAAGCGCAGCCGC
GAGTCGCCCCCTGTGCTGGGGCTGCGGCTGCTGAGCCGTTTCGCGCTCGGAGGAGCGCGGC
CCCTTCCGTGGGGCCGAGGAGGAGTGGCATATACCGGCCAGCCCCGGCGGGGACCCCCG
CTGGAGCTGGTGCACGGCCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTGGA
GAGCCTGGCCTCGTCCGCGCCTCTCGCTGTCACTGTCCAGCGGCTGCGGCGGACCCCT
CCCGCGCAGCGCCACCCGGCCTGGGAGGCCCGCGCGGGGACGGAGAGAGCTCGGAGGGC
GGGAGCTCGGCGCGGGCTCCCCGGTGTGCGGATGCGCAGGCGGCTGAGCTTACCCTG

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FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCTG
GGCCGCAGCACGCCGCTGTTTCGGACGGCTTCGCAGGGCCACGTCCGAGGGCGAGAGTCTG
CGGCGCCTTGGCCTTCCGCACAACCAAGTTGGCCGCCAGGCCGGCGCCACCACGCCTTCC
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTCCGGGCTCCTCAGCCCCAGGGGAAAGC
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTATCGCCACCA
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTACCAAGTACGTGCGCAGTGAGTCAGAC
TTCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGGAGGCAGCC
ACCCTGCTCTGCCTGCCAGCGGCCTGCCCTGCACCCGCACATCTCCTGGATGAAAGACAAG
AAGTCCTTGAGGTGAGAGCCCTCAGTGATCATCGTGTCTTGCAAAGATGGGCGGCAGCTG
CTCAGCATCCCCCGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCGAGTCCCAGGAAAGCTA
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGTGTGGAAGCCGGGA
GACAGCCGGGCACCTTGCACGTATACGCTGGAGCGGCGAGTGGATGGGGAGTCTGTGTGG
CACCCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCGTGTGGGCAGGGGGCCCTTCAGCAAC
TCTTCTGAGAAGGTCTTTGTGAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGCTGCC
CACCAAGAGGGCCCTGTACCTCAAGGCCAGCCAGGGCCCGGCCTCCTGACTCTCCTACC
TCACTGGCCCCACCCCTAGCTCCTGCTGCCCCACACCCCGTCAGTCACTGTGAGCCCC
TCATCTCCCCCACACCTCCTAGCCAGGCCTTGTCTCGCTCAAGGCTGTGGGTCCACCA
CCCCAAACCCCTCCACGAAGACACAGGGGCTGCAGGCTGCCCGGCCAGCGGAGCCACC
CTACCCAGTACCCACGTACCCCCAAGTGAGCCCAAGCCTTTCGTCTTGACACTGGGACC
CCGATCCCAGCCTCCACTCCTCAAGGGGTAAACCAAGTGTCTTCTCTACTCCTGTGTAT
GTGGTGACTTCTTTGTGTCTGCACCACCAGCCCCCTGAGCCCCCAGCCCCCTGAGCCCCCT
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCGGCCAAGGAGGTGGTCAGCTCC
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCTGAGGGTACCACTCTTCGACAGGGTCCC
CCTCAGAAACCCCTACACCTTCTTGAGGAGAAAGCCAGGGGCCGCTTTGGTGTGTGCGA
GCGTGCCGGGAGAATGCCACGGGGCGAACGTTCTGTGGCCAAGATCGTGCCCTATGCTGCC
GAGGGCAAGCCGCGGGTCTGCAGGAGTACGAGGTGCTGCGGACCCTGCACCACGAGCGG
ATCATGTCCCTGCACGAGGCCTACATCACCCCTCGGTACCTCGTGCTCATTGCTGAGAGC
TGTGGCAACCGGGAACCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC
GTGGCCACTTACATGGTGCAGCTGTACAAGGCCTGGACTACCTCCACGGCCACCAGTG
CTCCACCTAGACATCAAGCCAGACAACCTGCTGCTGGCCCCCTGACAATGCCCTCAAGATT
GTGGACTTTGGCAGTGCCCAGCCCTACAACCCCCAGGCCCTTAGGCCCTTGGCCACCGC
ACGGGCACGCTGGAGTTTCATGGCTCCGGAGATGGTGAAGGGAGAACCCATCGGCTCTGCC
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGAGCGTCCCCGTTT
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCCGCTTTGATGCCTTC
CAGCTGTACCCCAATACATCCCAGAGCGCCACCCCTCTTCTTGCGAAAGGTTCTCTGTGA
CATCCCTGGAGCCGGCCCTCCCTGCAGGACTGCCTGGCCCCACCCATGGTTGCAGGACGCC
TACCTGATGAAGCTGCGCGCCAGACGCTCACCTTCACCACCAACCGGCTCAAGGAGTTC
CTGGGCGAGCAGCGGCGGCGCCGGGCTGAGGCTGCCACCCGCCACAAGGTGCTGCTGCGC
TCCTACCCTGGCGGCCCTTAGAGGCACGGACCACAGCCAGGCCTCGGGCTTCAACTGGGG
TTCCACCAATGCCACGGGACATTCCAGGGCCACGCTGAGCCAGGCGGGCTGGGGCTT
CGGTTACCAACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA
GACCCAGGGCCTGGACCTGATGCCACCCAGGCCAAAGCCAGAGTGGGAGACCCATTGG
TCAGGCTCAGCAGGGTGGGAACAGGCAGAGGGACAAGAGGGGAATGGAGAAGTGGAGAGG
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTGGGGGTGAGT
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC
CCAGGTGTGAGGGCAGTAGGCTGGGAGTCAAGTGTGGCAAAGCGGGGGCAGGACACAGATA
CAGTGGCAGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGGCGGCAGAGGGAGAAG
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGTGTGAGCATCCCTCAGAGGAGAAATGTG

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FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCTCCTGTCCAGTGGATACAGC
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCCCTCCATGGCCTTTGGCCTTCT
TCCCATTTCATATTTATTTATTTATTGACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT
ACTGCCCATGTTGTCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA
AGGAAATAAAAATGGCAAGCAGCAAAAAA

SEQ ID NO: 43_AA542015_M SGK088_M

GCCACGGACATCTGGGGAGCGGGTGTGCTCACCTACATCATGCTTAGTGGGTACTCCCCA
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGTTCGCTTTGATGCC
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGGTCCTCTCA
GTACATCCCTGGAGCCGGCCCTCTCTGAGGACTGCTTGGCCACCCATGGCTGCAAGAT
GCCTACCTGATGAAGCTGCGCCGACAGACTCACCTTACCACCAACCGGCTCAAGGAA
TTCTCTGGGCGAGCAGCGGCGACGTGCGGCTGAGGCTGCTACCCGTCACAAGGTGCTGCTC
CGCTCCTTACCCTGGCAGCCCCCTAGGTGGCAGACCGCAGCCCGGCCACGGGCTTCAACT
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTACCCCGGCCATA
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAAGA
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT
TAGGCTGGAGTGGAAATGCTATATCTCAGGGAGAAGCCAGAAGGGGACATGGCTGAAGAGG
AAGAAGGACCCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC
CAGGAGCCAGAGCAGAGACATAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAAG
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC
ACTGGCCCAGGGATGTCCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCCATTTGTAT
TTATTTATTTATTGCCTTTTGTGGAGTTTCTTTCTATCCAGTCCCTAGTGCCTATGTTG
TCCCGACCATCCCCCTTCAGTCACCCAGCTGTCTGTGCAGCTGTCTGTCTGTCTGTCTCACA
AGGAAAATAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAGC

SEQ ID NO: 44_R19772_H

ATGAAGGGCGGCGACAGGGCTTACACCCGAGGTCCCTCTTTGGGGTGGCTCTTTGCTAAG
TGCTGCTGTTGCTTCCCGTGTAGAGATGCATACTCTCATTCTCAAGCGAGAATGGAGGC
AAGTCCGAGTCCGTAGCCAACCTGCAGGCCAGCCCTCCCTGAACCTTCATCCACAGTTCC
CCGGGTCCCAAGCGCTCCACCAACACTCTTAAGAAGTGGCTGACGAGTCTGTGCGTCCG
CTCAACAGCGGGAAGGCAGATGGAACATCAAAAAGCAGAAGAAAGTTTCGCGATGGTCCG
AAGAGCTTTGACCTGGGATCTCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCACACACACCC
CTCCCACCACCTATGAAGATTTTGTACAACGACCCTACACAGGATGAAATGTCCTCCTCT
TTGCTAGCAGCCCCGCGAGGCTTCCACTGAAGTACCTACTGCTGCAGACCTTGTCAATGCA
ATAGAAAAGTTGGTCAAAAACAAGCTGAGTCTAGAAGGAAGCTCATACCGGGGGAGCTTG
AAAGACCCTGCAGGCTGCCTGAATGAGGGGATGGCCCCACCCACACCTCCTAAAAATCCA
GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGAATGAGCTGGTA
CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA
ATAGAAGAAAAGGGTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTGTTGAAAT
ATTCATCAGATTTATGACTGGCATAAGGATTTTTTCTGGCGGAACCTGGAAAAGTGTATC
CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCTAC
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGACTTCCTCATCAAG
CCCATTCAGAGAATAACAAAATACCAAGTTGCTCCTCAAGGACTTCCTGAGATACAGTGAG
AAGGCTGGTTTGGAGTGTTCAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTC

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FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG
CAGTCCCGGACCAAAGAGAGGGCGGTGTTCTCTTCGAGCAGATTGTCTCTTCAGTGAA
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAGGAGCATCAAGATGAAT
TACTTGGTCTTGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACATCAAGACAGA
GAGACTTCTGAGAGGGTTGTTCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTTGAATGCACTGCAATCGCCC
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT
CCCCAAGCCAGCCCCAGGCCCTACTCCTCTGTTCTCGGGCTCAGAGAAGCCCCCAAAG
GGCTCCAGCTATAACCCACCTCTGCCTCCCTGAAGATATCTACCTCCAATGGCAGTCCA
GGGTTTGAATACCACAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCTCGCCGTCAACCAGCAGAACATGTGT
CTGGTGTACCAGCCTGCCAGCGACCATCCCCCGCCGCCGAGGGCTGGGTCCCAGGCAGC
ATCCTGGCGCCCCCTACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG
TCATGTTTCATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGGAGAACACGGGTAAA
AATGAAGCCACAGGGCCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTTAAA
GAGACGAACAGTTCGAGGAATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG
ATCTTAAATCCAAATTTTCATCCAAGAAGTGGCCCCAGAATTCCTTGTGCCCTTGGTGGAT
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAAG
CCCACCATCACTTGAAGGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC
ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCTGAAGATCTGTAATCTGATG
CCCCAAGACAGTGGGATTTATACCTGCATAGCAACAAATGACCACGGGACCACATCAACG
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCCAGGAG
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAACTGCACT
ATTTCTGGTTACACTGTGGAGTACAGAGAGGAAGTTCTCAGATCTGGCAGCAGTCAGTG
GCTTCGACCTTGGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGTGTCTTATCAG
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCAGCGAGCCCTCGGAGTTT
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCATTCTTGAAGGAAAAAT
TTTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCCGTTTCTCTATAGTAAAG
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTAAACAAAAAATG
AAGAAGAAAGAACAGGCTGCCCACGAGGCTGCCCTGCTTCAGCACCTACAGCACCCCCAG
TACATCACTCTCCATGACACCTATGAGTCCCCACATCCTACATCCTGATCTTGGAAGT
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAAA
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACAAGTGCAGGGTT
GCACATTTGGACATAAAGCCTGAAAACCTGCTCATTGACCTACGGATTCCAGTGCCTCGA
GTGAAGCTCATTGACTTGGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTACCAC
CTGCTGGGGAACCTGAGTTTGCTGCCCCAGAAAGTCAATCAAGGCATCCCCGTCTCCCTG
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTGATGCTGAGTGGGGTCTCCCC
TTCTTGGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTAGCTTC
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTTCATCAATGTGATCTTA
CAGGAAGATTTTCGGAGGCGGCCACAGCAGCCACATGCTTGACATCCATGGCTGCAG
CCCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCTAGCATGCTTCATA
GAACGTGCAAGCACCAAGATGATGTGCGGCCTATCCCCAATGTCAAGAGCTACATTGTC
AACCGGGTGAACCAAGGGACGTAG

SEQ ID NO: 45_5R72_8_2_H

CGCCGCTGTTTGTCTCGCGCGGCCCTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA
AAGTTTCTCCCGGTGCAGAATTCCGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT
GTCGGAGACCCGCCAGTCCGCCGGCCCCGGCTTTGTTTCGTGCGGAAGTGTAGTGGTGAGA

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FIGURE 2KK

AAAAC TCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC
TGGGCTGTACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAGTTC
GAAATTACAGTTTTTACCATCAACTACCTTATCCTTTTTTGGCCTGGTTTTCTTCTCAA
CAGTGGAAACATTTTTAAAGTTGCTTTTGTTCAGAGTTAAACAAATGGCTGATAGTGGC
TTAGATAAAAAATCCACAAAATGCCCCGACTGTTTCATCTGCTTCTCAGAAAGATGTACTT
TGTGTATGTTCCAGCAAAACAAGGGTTCCTCCAGTTTTGGTGGTGGAAATGTCACAGACA
TCAAGCATTGGTAGTGCAGAATCTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA
GCATCTCAGCAACAATGGGGTCGGGGCAACTTTACAGAAGGAAAAGTTCTCACATAAGG
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTGGAAGAATATTGGGAAAAGGG
AGCTTTGGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTAA
AAAGTGAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC
ATTCTGAAAAGTGTAACACATGAACACATCATACATCTGGAACAAGTATTTGAAACGCCA
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAAGTCAAAGAAAATCTGGAT
AGGAAAGGGCATTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAAATATAATG
GTTAAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG
ACTCCTATCTATATGGCCCCTGAAGTTATCAGTGCCACGACTATAGCCAGCAGTGTGAC
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCTTTTTGGCA
AGCTCAGAAGCGAAGCTTTTTGAGTTAATAAGAAAAGGAGAACTACATTTTGAAAATGCA
GTCTGGAATTCATAAGTGAAGTGTGCTAAAAGTGTTTGAAACAACTTATGAAAGTAGAT
CCTGCTCAGGAATCACAGCTAAGGAACTACTAGATAACCAGTGGTTAACAGGCAATAAA
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAAATAACCCA
GAAAGTGGTGAAGAAAACACAACAGAAGAGAAGAAATAAGCCGTCCACTGAAGAAAAGTTG
AAAAGTTACCAACCCTGGGGAAATGTCCCTGAGACCAATTACACTTCAGATGAAGAGGAG
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCTTGCAACCAGTAAGGACAACCTTGAT
ATGTGCAGTTCAAGTTTCACATCTAGCAAACCTCCTCCAGCTGAAATCAAGGGAGAAATG
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC
GCCCTGTCCAGAACCAAAAAGAACTCTAAGGTTCCTCCAGTGTGGACAGTACAAAA
CAAAGCTGCTCTTGTTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG
CTGAGCTTGAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTTGACACAGCTTAAAT
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAAGGACAGCCACAG
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTACTTCAAATCT
TATGTTTAGGCACAGCTATTTATAGGGGAAAACAAGAGGGCCAAATATAGTAATGGAGGTG
CCAAATAATTATGTGCACCTTGCCTAGAAAGACTTTGTTAGAAAATTACTAATAAACTTG
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTACATGTGTTTCGTGAGATTTTAGGTT
GCTATAGATTGTTTAAGACAGCTTATTTTAAATGTAGAAAATAGGAGATTTTGTAAGTG
CTTGCCATTAACTTGCTGCTAAATTCCTAATGTATTGATTAAATCAATAAAAAACAGATG
TTACTC

SEQ ID NO: 46_SGK309_H

GGGTCCGCAGCCCGCCCTCACAGGCCCTCCTCACTCCCCTAGGTAGATGGCCCCCTCAGG
GCAGGCCCCGGCGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCGCCCTT
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCCTGCCGGCCAACTAC
GTGGTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGGCTTTGGTGAGATC
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCAG
CAGCCCAAGCAGGTCCTCAAGATGGAGGTGGCCGTGCTCAAGAAAGTTGCAAGGTTCCGGC
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGGAAGGAC

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FIGURE 2LL

CATGTGTGCAGGTTTATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG.
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG
AGCACCACATTGCGGCTGGGCAAGCAGATCTTGGAGTCCATCGAGGCCATCCACTCTGTG
GGCTTCCTGCACCGTGACATCAAGCCTTCAAACCTTGCCATGGGCAGGCTGCCCTCCACC
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG
GATGTGCGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTTCGCTATGCCTCAGTC
AATGCCCCACAAGAACCAGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG
CTGGTGGAGTTTGCAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA
GGGATGATCAAGGAGAAGTATGAGCACCAGGATGCTGCTGAAGCACATGCCGTCAGAGTTC
CACCTCTTCTGGACCACATTGCCAGCCTCGACTACTTCACCAAGCCCCGACTACCAGTTG
ATCATGTGAGTGTGAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT
GACTGGGAGAAGGCAGGCACCGATGCCCTCCTGTCCACGAGCACCTCTACCCCGCCCCCA
GCAGAACACCCGGCAGACGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCCTGG
GGACCTGCTCCGGGAGAACACCGCGGATGTGCTACAGGGAGAGCACCTGAGTGACCAGGA
GAATGCACCCCCAATTCTGCCCGGGAGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT
TGTCCCCACCCCGGGGTCCTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA
CAAACCTCCGGATCAACATCGGCAAAGTAACTGCCGCCAGGGCGAAGGGCGTGGGTGGCCT
TTTCTCTACCCCCGATTCCCAGCCTTGTGCCCTGCCCTGTTCTCTAAGCACCTGT
CCCCCGCAATCTCCCTGCTTGCCCGGCCCTCTGTTTCCGGTCCCCTCCCCGGCACTAGCC
TCGCTGTGTCTTCCATCATCATCTCTGTCTCTTCACTGAGGAGACCATCCGCC

SEQ ID NO: 47_AA234451_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAACAGCAGC
AGCAGCCGCGCCGCGCCGCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCGCCGCGAGTCGGCGGTGGGGGATGGGCAGGCA
GTGGCGGTCCCGCTGCCGAGGGTTAACCCCGCGCGTCCCGGTCTGAGCTGGACCAGA
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCAGGTTAAATGGAAACCACCTTGG
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA
GAGCAGCTGGATATCCTGAGTGTTGGAATCCTAGTGAAAGAAAGATGGAAGTGTTGAGA
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGGACATGCTCACCAGGGAA
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT
GCTGTTTTGAAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTATTGGCTGTGGGAGG
AATGATCGATTCAACTATGTGGTCATGCAGTTGCAGGGTCGGAATCTGGCAGATCTTCGC
CGTAGCCAGTCCCGAGGCACATTACCATTAGTACCCTCTCCGGCTGGGTAGACAGATT
TTGGAGTCTATTGAAAGCATTCACTCTGTGGGATCTTGNCAATCGAGACATCAAACCGTCG
AACTTCGCTATGGGTGCTTTCTTAGTACATGTAGGAAATGTTACATGCTTGATTGTTGGC
TTGGCTCGACAATTTACCAATTCCTGTGGTGACGTGAGACCACCTCGAGCTGTGGCAGGT
TTTCGAGGGACAGTTCGTTATGCATCAATCAACGCACATCGGAACAGGGAAATGGGAAGA
CATGATGACCTTTGGTCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCCC
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAAGGAGAGATATGACCACAGG
CTCATGTTGAAACATCTCCCTCCAGAATTGAGCATCTTTCTAGACCATATCTCTTCTTTG
GATTATTTTACAAAACAGACTACCAAGCTTCTTACATCCGTGTTTGACAATAGCATCAAG
ACTTTTGGAGTAATTGAGAGTGACCCCTTTTGAAGTGGGAGAAGACTGGAAATGATGGCTCC
CTAACCAACCACCTACTTCTACCAACCCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAATACAGATGAG
GTATTTCCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA
GATAAATTGCCTGGATCTCTGGGACACCCCGTCCCCAGGAGAAGGATGTTTGGGAAGAG
ATGGATGCCAACAAAACAAGATAAAGCTTGAATTTGTAAGGCTGCTACTGAAGAGGAG
AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTTGGGTACCAATTCGT

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FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCTACTGGTGCGAAAAGTTACGTTCC
ATTACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG
TTCCTTGAGACCTGGTATAAAATAGTGATTTTTCTTTTTAAAGCTTCTAAGGTACCATT
ATTATTGTTGTCAATTGTTGTTATTATTATTGTATATTTCTGTTACATAAAAGTCTTTCAA
TAAGAAATCCTTGCATTTTTTGTAACACTGAGTCTATTGAGCTCCAATTTTCATCCATGTT
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCCTAACACTAGGTACAAGTTAAATGAACAT
TTTTACAGTAACTTTGTTTAGAAAGTAATCTCTCCACACAACAGTGAGTGCTGGAGAG
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT
AATTCATACACAAGGGACGGTGAGTTCAATTCACTTTAGTGAAGACCCTCTAGGAGTAAG
ATACTGTGGGAAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG
TGCATGGTTTTGAGGCACATTATCCCTACAACAAATTTTGATAACAGAAGAC

SEQ ID NO: 48_AA435956_H

ACTTTTACTATATTCTTTGAGATGACTGTTTTTGATTTAGAGGCGAAATCAGCACGTGGT
GGCTCAAATCTCCTTATGGATAGTGTTTCTTCTTCCAGCTTTTCATGTTTCAACTTTTG
CGGGGCTGGCGTACATCCACCACCAACACGTTCTTCACAGGGACCTGAAACCTCAGAAC
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCGGGCCAAG
TCCATTCCCAGCCAGACATACTCTTCAGAAGTCGTGACCCTCTGGTACCGGCCCTGAT
GCTTTGCTGGGAGCCACTGAATATTCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCTGGGGTTTCCAACATCCTTGAACAG
CTGGAGAAAACTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGCGCGGGAGTCTCC
AAGCTACCTAACTACAATCCAGAATGGTTCCCACTGCCTACGCCTCGAAGCCTTCATGTT
GTCTGGAACAGGCTGGGCAGGGTTCCTGAAGCTGAAGACCTGGCCTCCCAGATGCTAAAA
GGCTTTCCAGAGACCGGTCTCCGCCCAGGAAGCACTTGTTTCATGATTATTTTCAGCGCC
CTGCCATCTCAGCTGTACCAGCTTCCTGATGAGGAGTCTTTGTTTACAGTTTCAGGAGTG
AGGCTAAAGCCAGAAATGTGTGACCTTTTGCCCTCCTACCAGAAAGGTCACCACCCAGCC
CAGTTTAGCAAAATGCTGGTGAAAAGAAAGGGCGAGATCACCAAGGTTCTTCAGGGCTGT
ATTTCTGCAGTTTCGGTTTTTCATTTGCTTCAGCTTACTAAGAAGCTTCAAATCTAACTCC
ATACTGAACAAGGGGCTTTATGTCTCACCTATGACCTGGAATAGTTTAAATATGGTGTT
CAAGGCAATAGTACATAATAGTGGAAGAAAAATTCAGTGGAAGGTTATTGCTATTGTGATT
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAACTAAGTCTAAGAAG

SEQ ID NO: 49_AA626859_H

AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA
TTTCTGTACATATACATAACTGTATTACAGAGATATAAAACCTGAAAATATTCTAATAAC
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGACAAATCTGATTCCAGGAGA
TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTTGGGAGA
TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGACAGAGCTCCT
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA
TGGCATCAGTATACCTGAGCCAGAAGACATGGAACTCTTGAGGAAAAGTTCTCAGATGT
TCATCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAA
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAAACAAGTCTCCAGTTAA
ATTTGATCACCTTCCAAACATTTAGGAAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT
GTACACATTTGTACAAGTGAGATAGGAATCTCAGTGTTTCAAATGCAAATGAGCCATA

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FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCCCTTTCCCCA
TGCTTTTACAT

SEQ ID NO: 50_AA061797_M

GAAAATAGCCCTGCGGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT
CATCGAGGTGTTTCAAGAAAGAGAAAGATGCATCTAGTTTTTGAGTACTGTGATCACAC
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAGTGT
GCTATGGCAAACCCCTTCAAGCCCTTAACTTCTGTCAACAAGCACAATTGTATTCATCGGGA
TGTAACCTGAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG
ATTTGCACGAATTCTAATTCCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA
CCGAGCCCCCGAAGTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGC
CGTCGGCTGTGTTTTTGCAGAGCTCCTGACGGGTGAGCCACTCTGGCCGGGAAAATCCGA
CGTGACCAGCTTTACCTGATCATCAGGACGTTGGGGGAAGCTGATTCCAAGACACCAGTC
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA
GACTCTTGAAGAAAAATTCTCAAATGTTTCAGCCTGTGGCTTTAAGTTTCATGAAGGGATG
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCAGCTGCTGGACAGTGCCTACTT
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAAGCCGAAG
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCCTGGAAGCCACATCTCCCCACACCTGA
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTTCGATCATCTTCCAAACATTTAGGGGACTCA
TCCTTCCCAGCACATCCTTTTAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA
TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC
CTGTGCTTTTTCCACGCCAGCTCCATCTCCTAAAACATTCTCTTTAAATGTTGCAGTATC
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTCACCAGAGCCGGGCTTCTCAGGCAA
TCGGTACTGTGCATCTGTGGACTTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT
CTCACTTCAGCCGACCAGTGGTGTCTGAAGCAGACCCAGATCTGCTGGCTGCTGTTTGT
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT
TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA
CGAAGTAGAGAAAATTCCAAACGTGACCAGTTAGTGGACAGACTACAAGGAATCGACCAC
CATACCACAGTAACGCCCCCTGGATCCCTGGCTGCCACCCACTCTAAGGCTATCCTGGTT
CACCATGGTTTCTCTTTCTTTCTTTCTTTTAAATCTATTTGTACATATGAGAAAGAGGC
AGAGGGGCGAGAGAAACCTCGTGTGTGAAAATCAAAAGACAAGCAGGAGGCCAGCCTAAG
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCCAAGTCCCT
GCTGCTGATTGTATAAACTATGAATAAGTTCTACATATGTAGGACATATTGTTGTCAATTG
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTTCTAAATATTCTCCACACTGGTG
AGTATCTTGGCATTTCATTTCTGACCTCATCACAGATGAACACATCAAAGGATGAGTATG
TATCACTTTGCATCTTAGAATTCTACCTGTTTTAGCTGCGTTAAACCTTGTGAAAGGGCG
GGGCCATAACTGAACCTGTGGAGTTCTTGCTGTGTGCAGGAAACCCCTCTGGTTTTGTCT
CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAAATTCAAAGTCACT
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGTACACTTCTCCAGGCATGAAGG
TCCGTGTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC
ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAACCTAATAGGAGTCGTTGAAGGTAG
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTAGTTTAGAAT
GCATTAAATGTATGTAGAAGCTGGGCTATTTTCAAGTTATTTGAAATTGTAGCTATTGTTAA
TTAGCACTTAATAACTAAGTAGCATTATGGTAGTCTAACTATTAGAGTTTACTACAAAG
AGGTTTTGATTGAATTATATTAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA
GAAAGCTATATAAAGATTAAACATTTTTGTGGCTGTATTTGTGTATATACCTTGGTTG
TTCTTTAAATTATTTTAAATAAAGCCAGAAACATT

FIGURE 200

SEQ ID NO: 51_AA397553_H

ATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAAC
TTGCAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG
AAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCCGAAGCA
GCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGT
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGG
GACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAGCCAAGAAGTCTCCAGCAAGTCG
GGATCGATGAAGGACCGGATATCGGGAAGTTCAAAGCGTTCAATGAGGAGACTGATGAC
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCATCCAAGCTCCAC
AAGGAGAAGACCAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAGT
CATCGAAAAAGGAAACACCCAAAAGTTACAAAACAGTGGACAGCCAAAACGGGAGATCC
AGGAGCCCCACAGGAAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCCTCGGGAGCT
TCTTACGGCCAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC
TCCTACAGGAAAAAGTCTTGAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG
GAGCCTTCGGCCTACCAGTCCAGCACCCGGTCACCGAGCCCTACAGTAGGCGACAGAGA
TCTGTCTAGTCCCTATAGCAGGAGACGGTCGTCCAGCTACGAAAGAAGTGGCTCTTACAGC
GGGCGATCGCCAGTCCCTATGGTCTGAAGGCGGTCCAGCAGCCCTTTCTGAGCAAGCGG
TCTCTGAGTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCTT
GCATATTCAAGACATTTCATCTTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGT
CATTCCAGTATCTCACCTGTGAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACCTCAGT
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCC
AAGGGTTACCTGTATTTTTGCTTAGAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTCA
GGTTTGGAGTCTAAAAAGTTACCCAGAAAGTGTAATAATTGGAAAAATCTGCCCCAGATACT
GAACTGGTGAATGTAACACATCTAAACACAGAGGTAAAAAATTCTTCAGATACAGGGAAA
GTAAAGTTGGATGAGAACTCCGAGAAGCATCTTGTTAAAGATTTGAAAGCACAGGGAAACA
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAAGGAGACAGAAACA
TCAGAAAAGGAGACCCCTCCACCTCTTCCACAATTGCTTCTCCCCACCCCTCTACCA
ACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCCTCAATACCAGCTCTT
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCTGCTTCCAGT
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGCTCTCTCAGGCAAAT
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAACAGCTGCTATTCCA
CACCTGAAAACCTTCAACGTTGCCTCCTTTGCCCTCCACCCCTTATTACCTGGAGGTGAT
GACATGGATAGTCCAAAAGAACTCTTCTTCAAACCTGTGAAGAAAGAGAAGGAACAG
AGGACACGTCACCTTACTCACAGACCTTCCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTG
TCTCCCCCAGACTCTCCAGAACCAAGGCAATCACACCACCTCAGCAACCATATAAAAAAG
AGACCAAAAAATTTGTTGTCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGG
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA
GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTTCGTGAAATCAAATCCTTCGTCAG
TTAATCCACCGAAGTGTTGTTAACATGAAGGAAATTGTACAGATAAACAAGATGCACTG
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTTGAGTATATGGACCATGACTTA
ATGGGACTGCTAGAATCTGGTTTGGTGCACCTTTTCTGAGGACCATATCAAGTCGTTTCATG
AAACAGCTAATGGAAGGATTGGAATACTGTCAAAAAAGAATTTCTGCATCGGGATATT
AAGTGTTCCTAACATTTTGTCTGAATAACAGTGGGCAAATCAAACCTAGCAGATTTTGGACTT
GCTCGGCTCTATAACTCTGAAGAGAGTCGCCCTTACACAAAACAAAGTCATTACTTTGTGG
TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG
AGCTGTGGATGTATTCTTGGGGAACATTACAAAAGAAGCCTATTTTCAAGCCAATCTG
GAACTGGCTCAGCTAGAAGTATGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG
CCTGATGTTATCAAACCTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

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FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTTCATTCTTCTGCAGCACTTGATTTATTGGACCACATG
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT
AAAGATGTGGAACCTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCAT
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTGTAGTCGAAGAGCCA
CCTCCATCCAAAACCTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG
AACAGCAGCCCAGCACCACCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG
ACGGAAGCTACTTCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG
GAAGCACCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCTTGAAGCTTCA
AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC
CAAGAGCCAGCAGGCAGTCTGGAGGAAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG
CCCCGAAGAACTCCACAATGCCACAGGAGGAGGCAGCAGCATGTCCTCCTCACATTCTT
CCACCAGAGAAGAGGCCCTGAGCCCCCGGACCTCCACCGCCGCCACCTCCACCCCTT
CTGGTTGAAGGCGATCTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC
TTGCTGCAACTTTTATCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC
ACTGATGGGCCTGAAACAGGGTTCAGTGCCATTGACACTGATGAACGAAACTCTGGTCCA
GCCTTGACAGAATCCTTGGTCCAGACCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAGTTTCCAGGGGAC
CAGGACCTCCGTTTTGCCAGGGTCCCCTTAGCGTTACACCCGGTGGTCCGGCAACCATTCT
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAAATTGCAAACTAT
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG
GGCCCAACTCAGTCTTCTGCTTATGGAAAACCTATCGGGGGCCTACAAGAGTCCACCA
AGAGGGGGAAGAGGGAGAGGAGTTCCTTACTAA

SEQ ID NO: 52_AA789239_H

TGAAATGGAGATGTATGAAACCCTTGGAAAAGTGGGAGAGGGAAGTTACGGAACAGTCA
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAGATATTTTATGAGAGAC
CAGAACAATCTGTCAACAAAATTGCGATGAGAGAAAATAAAGTTTCTAAAGCAATTTTCATC
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCATTTGGTAT
TTGAATTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTGATGGACTAGAGA
GTAAGCGACTTAGAAAATACCTCTTCCAGATCCTTCGAGCAATTGACTATCTTCACAGTA
ATAATGTAATCATTTCATCGAGATATAAAACCTGAGAATATTTTAGTATCCAGTCAGGAA
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAGAGATACTTCTT
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA
CTGGAAATCCCTATCTTCCTAGTAGTTCTGATTTGGATTTACTCCATAAAATGTTTTGA
AAGTNGATTTCATGCCAGAACTGAAAGCTAAATTAAGTGCAGGAAGCAAAAGTCAATTCAT
TAATAAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAAACAG
TTTATACCAATACACTGCTAAGTAGTTTCAGTTTTGGGAAAGGAAATAGAAAAAGAGAAAA
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAAGTCAAAGGAGGAAGAGGAGATATCTCAG
AACCAAAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTTC
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATTGAACCACCAAACCTATCAATCCCA
GCACTAACTGTAATGGCTTGAAAGAAAATCCACATTGCGGAGGTTCTGTGACATGCCAC
CCATCAATCTAACTAACAGTAATTTGATGGCTGCAAAATCTCAGTTCAAATCTCTTTCACC
CCAGTGTGAGGTAACTGAAAGAGCAAAAAAGAGACGCACTTCTTCACAATCTATTGGAC
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCTTATTCAAAGCCAAATGGAGAAGG
GTATATTTAATGAGCGAACAGGTACAGTGACCAAATGGCAAATGAGAACAAAAGGAAGC

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FIGURE 2QQ

TGAATTTTTCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC
AAGAGTTTATTCCCTTATCTCTGCTGTCTGCCTGCTGTCCTATTTTTCACAAATATTTGCT
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG
GTTTTTTTTTCTGGTAGTGTCTTTTCTTTTACATAGTCCAAAAAATACAAGATGACAACCTC
TTCCCGTTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC
ATGTGCATGAGCATCATCCAGCTTTTTTTTGTAGCAAAACATTTACTGTTTTCTTTTCCC
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC
CTTGAA

SEQ ID NO: 53_AA124976_M

CTGGCAGATATAGTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT
GATCTTTTTCGCTCACGATTACTTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTAAATTCATTTATAAAGCCAAAAGAGAAT
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTTACCAACACCCTGCTC
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCAGACCAGAAGAAGCCA
GAGTATGAAGGCGACCACCGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCCAGTGAGAATTCTGAC
GGTGTCAAAGAAGACCCACACGCTGGGGGTGTATGATAATGCCACCTATCAACCTGACA
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCACCCCAATTCACGGTTA
ACTGAAAGAACAAAAAGAGACGCACTTCTTCAAACTATTGGACAGACTTTGTCTAAT
AGCAGACAAGAGGACACAGGTCCACACAAGTCCAAACAGAGAAAGGTGCATTTAATGAG
CGAACAGGTGAGAAATGACCAAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA
TGCGACAGGAAAGAATTCCATTTCCCTGAACTGCCATTACAGTGCAGGCGAAGGAGATG
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTTCCCGATAGTGCTTT
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTTATTTTATATAC
ACTAGAATGTACATAGGTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT
CTATTTTTTTTGGTTTTGCTAGCAAAATTTTCAAAATTTTTCTCTATCTTCCAAAACTGT
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA
CATTCTATTGTCCCCAGTGAAGCATTTATAGTACTTACATAACATGTTACAGTGATATGA
TGTTCCTAGGTTAACTCCTTGAGATGAACTATTTCCCTGCATTCTCTGACTCCCCTAGT
CTAATAGTTCCCTTCCATTTAGCCAGAAGAATTTCCCTGAAGAAGCGATGCACAACCTGGGA
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA
GTTAACAT

SEQ ID NO: 54_AA575635_M CCRK_M

AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCGGGTCTTCTCTCCGGAT
GGTGGTTCGCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACTGTGCTGT
GTGCTTCGCATCCTGGGTACCCCGAGTCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAGTGCCCTGGAGGAGGTGCTGCCT
GATGCCTCTCCCCAGGCCTTGGACCTGCTGGGCCAGTTCTCCTCTACCTCCACGACAG

7/11/03

FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC
CATCCATCCGAGCTGCCAATTCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC
CCAGAACTGATTGGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCCTCCTGCT
CGCCCTAGGAGCACCTCTTTCTGATTTGCCTCCATGGCCTCCCCACGGCTATATATACCA
CACCTGGTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA
TGTTTCATCCCAGCAGAGAAAGAGACTCACGTCTACAGACAAAGCCTCCAGAACTGCTA
GCTGTGTCCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC
AGGCTCTGTCCCCTCTTCAAGGACATTGGTACTACAGCACCACTGGTGGAAGCACAGAG
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT
CCACTGGGTGAGGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTTCTGTCTAATTGCACC
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTACAGGGGTGAGGTACT
CAGAAGGGGCCTCCTGTGAAGGCCATTGTTGGTCTCAGGCTTCCCATGCTATTCACGGGA
CTTGAGTGCTCATTGAGGAGCGAGGGTCCAGAAGCTGAGGCCAGGGATGGACAGTCCAG
TTCCCGAAGCCCACTTCCACATGTGCGGTGGGTGAGTCACTGAGCCTGAGGCTGCCTTG
CAGATGCGGAAGCAGGCATTCTTGAATCCACTCAGTAAATAAATTCCAGTGTGACTCAG

SEQ ID NO: 55_AA631990_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA
TCTGGTCACTCACTATCCATTTCATGATTACAACCTTCAATACTATCGCGGCCGAGGA
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG
CGGCATTCCAAAAGAACTCACTGTCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTGCTATTATTTAGAAGCAAGGTCC
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT
GAAGGATATGTTCTTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGC
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCTAAAAGGAAGCGCAATAGACACTGT
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGACACTTTGGGTGAAGGAGCCTTTGGC
AAAGTTGTAGAGTGCAATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAAATCGTA
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTTCAGAAATCCAAGTATTAGAGCACTTA
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT
CATGGTCATGTTTGTATTGTGTTGAACTACTGGGACTTAGTACTTACGATTTTCATTA
GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC
CAGTCAATAAATTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAA
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
CTTGGTTTTCAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
ATATTAGGACCCATACCACAACACATGATTACAGAAAACAAGAAAACGCAAGTATTTTCAC
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC
AAACCGTTGAAGGAATTTATGCTTTGTGTCATGATGAAGAACATGAGAACTGTTTGACCTG
GTTTGAAGAATGTTAGAATATGATCCAACCTCAAAGAATTACCTTGGATGAAGCATTGCAG
CATCCTTTCTTTGACTTATTAATAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA
CTTCTCTAGAAGAGATTACTTAAGACTGTGTGAGTCACTAAACATTCTAATATTTTGT
AAACATTAAATTATTTGTACAGTTAAGTGTAATATTGTATGTTTGTATCAATAGCAT
AATTAACCTGTGAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAATTTT
TCTTTTGAATTAACATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT
GTGATTGATCTTGCCCTTTGTACATGGAGGTCACCTCTGAAGTGATTTTGTGAGTAA
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

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FIGURE 2SS

ACTTAACTTTTAAAAGTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAG
ATAAGCAGGTACTAGAAACCAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT
TTAAGTGTGTATTCTTTTTCATTGGGTGATGTGAGGGTGATAACCAGACATTCATGGAA
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAAACACATACACACTTTATTT
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTAT
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA
TTGGTTACATAAACTTTTTGACTTCAAT

SEQ ID NO: 56_AA557536_H

AGTAAGGCCCCGCGGGCGTCTGGCCGCCATGTGCACCGTAGTGGACCCTCGCATTGTCC
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCCTGCCCAGGTACAGATCTCTCCA
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCCTCCTGGCCTTCCAGCC
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTGTTGAGTTTATGGACACTGACC
TGAACGCAGTCATCCGGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT
ACCAGCTCCTGCGGGCCACCCGGTTCCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA
AGCCGTCCAATGTGCTCCTGGATGCCAAGTGCACAGTGAAGCTGTGTGACTTTGGCCTGG
CCCGCTCCCTGGGGCAGCTCCCTGAGGGGCTGAGGACCAGGCCGTGACAGAGTACGTGG
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTTCGCACCGCTACACCGCTTCCT
GCCCCAGATACACCTTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC
TGCGGGGGAGACCCCTGTTCCCCGGCACGTCCACCCCTCCACCAGCTGGAGCTGATCCTGG
AGACCATCCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC
CGCCAGACACCTCCCCAGAGGCCTTGGACCTCCTTAGGGCGACTCCTGGTGTTCGCCCCGG
ACAAGCGGTTAAGCGCGACCCAGGCACTGCAGACCCCTACGTGCAGAGGTTCCACTGCC
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCGGGCACACGAAGGGGTCCAGC
TCTCTGTGCTGAGTACCGCAGCCGCGTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA
GCGGCACCTCGAGAGAGAAGGGCCCGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA
AAGCCAGAGCCGACCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC
CCCAGAGCAGCCAGGCCATGACCTGCGGAGCACGAGTCCCCCGTGCAGCCAAGAAGC
TTCCAGGCAGAACTCCGCTCCCCCTGCTCCAACTGCTCTCCTAGGGAATGGGGAAAGGC
CCCCGCGGGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG
GAGCTGCGCCCTCCCTGACCTCCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC
GGGTGACTGGAACCGGGCGGTGGGGTGAGGGTGCCAGCGTACAACAGGTCCCTCCCC
GGCTTCCTCCGAGGCCCGGCCCGGCGGAGGATGTTACGACCTCTGCCTTGCAAGGTG
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC
ACTCGGCACTGGGCCACCTGCCCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC
CTTACCTGGCCCTCTGTTCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCGTTGAAGTTCCAGGGAGCTTGCCCGGT
CTCCTCGGGGGAGCAGATGAGGGCCCTGCC

SEQ ID NO: 57_N28606_H, MOK_H

ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAACGTTTTCTGAAGTTATGAAG
ATGCAAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAA
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGCACTA
ATATGTGAACCTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

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FIGURE 2TT

TCAGAAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTAC
AGAAATGGAATATTTACAGAGATGTAAACCAGAAAATATACTAATAAAGCAGGATGTC
CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCC
CTCTTTCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTCTATCGGCACA
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCTCT
TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCACCAGGCCCTG
CAGCACCCCTACTTCCAAGAACAGAGGAAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA
AAAGCTGGCTTTCCGGAGCACCTGTGGCACCGGAACCACTCAGTAACAGCTGCCAGATT
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA
CGAGGACCGGCCTATGTCATGGAACCTGCCCAAATAAGCTTTCCGGAGTGGTCAGACTG
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG
CCGGTGCTGAGACCCCTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC
CTTAAGCCTGCCCCGCAGCAGTGTGCGCTGCCACCATAGTGCAGAAAGGCGGAAGATAA

SEQ ID NO: 58_AB023153_H, ICK_H

ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCTGTCTG
GGAAGAAGCATTGAGTCTGGGGAGCTGATCGCTATTAAAAAATGAAAAGAAAATTTTAT
TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAGAAGCTCAACCATGCC
AATGTAGTCAAATTAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG
TACATGAAGGAAAATCTTTACCAGCTCATTAAAGAGAGAAAATAAGTTGTTTCTGAGTCT
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTCACAAACTCGGC
TTCTTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA
ATTGCAGACTTTGGTTTGGCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGTCCCCC
ATTAGCGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAAA
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACTTCCGTTGGCCACAG
TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACCTTCGA
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCAACAAAACCTTCAGGATTCA
GAAAAACACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAGCCAGTC
CCACCTGCCCAGCCACCAGCCAAGCCACACACGAATTTCTTCAGCAGCATCAAGCC
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCGTTGCTTTTCCCATCCCTCCACAACAAG
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAATGGTGAGATAAAGCCAAAG
AGTAGGAGAAGGTGGGGTCTTATTTCCAGGTCAACAAAGGATTGAGATGATTGGGCTGAC
TTGGATGACTTGGATTTAGTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA
CAGAGTGATGACACTCTCTGCAGGTTTGAGAGTGTTTTGGACCTGAAGCCCTCTGAGCCT
GTGGGCACAGGAAACAGTGCCCCCACCAGACGTATATCAGCGGCGAGACACGCCCCACC
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCCCTGGGATCAGT
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCCACCTAATCCATGGTCT
AGTTCTGGCTTGTCTGGAATCTTCAGGGACAATGTGAGTAATCAGCAAAGTAAATTCA
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAACTATGTCCCTTCTTTCTG
AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCCAGACCCCTCC
CCTGGTTATTCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATTCTTGACACC
CAGCCTAGAAGCACTCCTGGGTTGATACACGGCCTCCAGCCGCCAGCCAGTGCATGGC
CGGACAGACTGGGCTTCCAAGTACCCATCCCGCGGTGA

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FIGURE 2UU

SEQ ID NO: 59_AA839940_M

AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG
CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCAG
GGCCCAGGAAGAACTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTTGAACACCGGGTAGTGAGCATCAAAGAT
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTCGGTTT
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG
CTCAGCCACGTAAACTTGATCCAACCTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTTGACCGGATCACGGATGAGAAGTAC
CACCTCACTGAGTTGGATGTGGTCTTGTTACAGAGGCAGATCTGTGAGGGTGTGCATTAC
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTGTCAGC
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATACAAGCCTCGG
GAGAAGCTAAAGGTGAACCTTGGTACTCCGGAGTTCCTGGCCCCAGAAGTTGTTAACTAT
GAGTTTGTGTCAATTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC
TGCAGCTGGGATTTGATGCTGATACCTTCAAAGGGCTGTGCGAGGAAGCCAAGCAAGCTTT
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTGCGCTCAGATCC
CAACAACCTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC
CACTGGGCCTGGGAATTTTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAATGATGGA
AGGAAGCAAGAAAGAAAGAAAAGAAAGGGGGAAGAAAAGGAAAGGCAGAAAGCAA
GGAAACAGGCTACGTTGTTGCTCTTCTTGTAGGTGAAAGTGTTTTTATTAAAGCCCTAG
GAATGTTTTTCTGCCTCGTAAGGTGAGCAGGTCTCATATGCTGCTTGCTACCCCGCACCC
TTCTTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAATCCTACTTGGCTTT
TGGTCAAATTTGAATTTCTAACTTGTCTATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA
TTCTTAAAGAATTAATAAAATATATTTTTTAAAGGAG

SEQ ID NO: 60_AA460132_H

GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAG
TGTCGGGGTGGACGCATTCGGGTAGCCGAAGAAGTCCAGGATTGCCGAAGAAGTCCCA
GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAGACAGCTGATCGGTTGGAG
CTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACGCCGCGCATGGCGAGGAG
CCCCCCCCGAGGCTGAGGCTCTGGCCGCAAGCCCGGAGCGGAGCAGCCGCTTCTTGAGC
GGCCTGGAGCTGGTGAAGCAGGGTGGCGAGGCGCGCGTGTTCGTGGCCGCTTCCAGGGC
CGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG
CGGCTTGGCAGACGGCGGACGGTGCAAGAGGCCCCGGGCGCTCCTCCGCTGTGCGCCGCT
GGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCCAACCTGCTTATATATGGAA
GAAATTGAAGGCTCAGTGACTGTTGAGATTATATTCAGTCCACTATGGAGACTGAAAAA
ACTCCCCAGGGTCTCTCCAACCTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC
GATGAAGACCTCATTCAATGGTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCATTTACGCACTTCCAGAG
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCTCAGTACCCATCCCCAACT
GAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCTCCAAAAAGGCCAGGCCA
GTGCTAAAAAAATTAGATGAAGTGCGCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG
AAGAATGTGTATGACAACCACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAAA

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FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTTAAGTGGTATGTG
ATCGTGTCAATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCAATGTTCT
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCAGATTGTGACATGTA
TATCTCAGATACATGGGTGTGGCATTGAACCACATAATGAGAACATTATTCTCTTTTTAG
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT
AACCAGTGTTTTTTTTTTGTGTTGTTGTGTGTACATGTTATATTTATTTTGAAACCAGTTT
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61 SGK034_H

CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG
GACACGGAGGAGGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC
TTCGCGGCGCACGAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGCTGGTGGACCAC
CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC
ATCTTCATCACAGAGTACGTGTCAATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG
AAGAACCACAAGGCCATGAACGCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC
ACCATCTTCATTTCAGCACAAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC
TCCAATGCACTTCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGG
AACCTGCACTTCTTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAATCCAGACCAATGGGGAC
ACCCGGGTACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG
CGGGAGTTCATCCTTTGCTGCCTGGCCCCGGGACCTGCCCGCGGGCCCTCTGCCACAGC
CTCCTCTTCCACCGCGTGTCTTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC
TTCATCCAGCACCACTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGAGGCCCGCTGCAGTGGCGG
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTGAGGAATGGAATC
TACCCACTGATGAACCTTTCAGGCCACTCGACCCCTGGGGCTGCCCGTGTGCTGGCCCCA
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCGACGCCAGAGCCCTTTGACTCTGAGACC
AGAAAGGTTCATCCAGATGCACTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT
CTCACTCTGCTTCTGGTGCTGGAAGACCGCTGCACCGGCAGCTGACCTACGACCTGCTC
CCAACGGACAGCGCCCAGGACCTCGCCTCGGAGCTCGTGCATATGGCTTCCTCCACGAG
GACGACCGGATGAAGCTGGCCGCCTTCCTGGAGAGCACCTTCCTCAAGTACCCTGGGACC
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGTGCCCCGGGACGGCC
ATGTTGGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAAG
GCCCCGGTAGTGAAGGAACCCCCCGTCTCCTGAGAGTGGGGCTGACCTGCCTTGGGCGC
CGAGGGGTGGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCAGGTCTTAGGATCAGG
GTTGCCCCCAGAACCCCTTCCCATATCCTCCATTCTCCGCCCTGAGTTCTTACCAGGCT
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCAGC
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCAGGGAACTGCTCCAT
GGGGTCTGGGAGAGCAGCCATCCCCCTGCTGGACCATAGACCCACACAAGGAGCCTGCAC
AGCAAGCCAGCGGTGACACACCTGCAGGTGTGAGGCATGGCACTGGGCACAACAGGGACC
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTGAGCAAGCCCCCT
GGTCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCCTGAGACCAG
AACTTGAGCCCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCCCTCAATGGGCTTTTTTC
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC
TCACAGCCCCCTCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCCTGGGCCCT
CTGAGGATGTGAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCCTGGCCTCTTGATTCTTGGCTT
GCCTCTCCTCCAATTCCAACTTAGTGAAATGGCCTTAAGCATTTTAACTGTATGTATA
CATTAGCGCATTTCATGCCTTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC

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FIGURE 2WW

TGTATTAGTTTTATACTGCCGCTGTAAATTTACCACAACTTAGTGACTTAACACAAAT
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG
CTGCTGGCAGAATCCACATCCTTTCGGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC
TGTAACCTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCTTGCTCTTGCCCCC
CTCCTCCATCTTCAGAGCTAGCAGGTTCACTCTGTGTACGAACCATTTCTCTGGTTCCC
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT
GCCATGTAACTAACATTCACTGGTTCCAGGGATTAAGGAATGAACCTCTTTTGTGGGG
AAGGTGGCATTCTGCTGACCACAGCACTCCAACCAAAAGCCAAAACCAAGCAAGACT
TACTAACGCATATCAAATAAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA
TTCCAATACTATTTACAAAATTATTCAAATTCTCACGCCCTTCCAACCTCAAATTAGCAAT
CTAAAGTAATTTCCATATCCTAGATGGAAACCCTCATGCTAAACTGTCTGATTATGCATG
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAAACTGAACTTAA
AAGC

SEQ ID NO: 62_AA103218_M SGK034_M

CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG
GGAATTCATCCTCTCCTGCCTGGCCCCGGGACCCTGCCCCGCCGACCCTCAGCCCAACCT
CCTCTTCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA
CCTCCATGCAGTTTTGGCTGAGATGCCGCAGCCCCATGGACCCCCAATGCAGTGGCGGTA
CTCAGAGGTCTCCTTCTTGAGCTGGACAAATTCCTAGAGGATGTCAGGAACGGGATCTA
TCCACTGATGAACTTTGCGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC
CCCAGAGGAAGCCCCAAAGGCCAAACTCCAACGCCAGAACCTTTGACTCGGAGACCAG
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC
AACGGACAGTGCCCAGGACCTCGCTGCTGAACTAGTGCATTATGGCTTCCTGCACGAGGA
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACCTTTCTCAAGTACCGAGGGACGCA
AGCGTGACCTTCCCAGTCTTGACGGCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACCTGAAC
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCAGCTTTCTGCAGCAGTGTGGGACCCT
GGGGTGGTGATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTGAGTTAGGGGAACCG
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCAGTAAACCTAGGGGAAGGAG
CCTGAACTCAGGTGTACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCCTTGGTCTGCTCA
GACCACTCCTGATCCCTTGACAGACCTGCCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT
GAGACCAGACCTGTGTCTCCTCCCCAAAGCCCTTGGGAAGGATCTTTCTATTTCATCATCCC
TCTGGCCTAGGGGCTCAGGGGTGAGGCATCCTCCACATTCCCTCCCTGGGGAAGTTGTGT
GTTTGAGTTGAGGATGTGGGTTCTGGCTCCCTCTTTCTCCCCAGCCCAACTTGTCTCTT
TCTTACTGGTTTCAAAGTCCTGATGAACGCTTCCCCTCAGAGCCACCCTGGTTTTCTTGG
TTCTTGAACTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTTAAATGCATAT
ATAAATGTAATGCAGTCACGGTCTCTTTTAAACACTTTTGTGTATGAAACCAGGAAAGCTC
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCCAGTGG
TTTGAGACGACACACACACACACACACACACACAGAGAGAGAGAGAGTTCTGTGA
CATCAAGTGTGATCCAGGCTCTCACTAGATTAAATACCCAGGCTAAGTTCTTTTCTGGAAG
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCTCTCAGCTTCTAGAGG

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FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT
CTTTGTCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCTTCTCAGGGTCTATAGATGAAC
CACACCTGCGCAGTTCCTTCTGCTGTCATCCTGGGCTTTGGTGCTTGAGAACAGCCGTG
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA
AATAAAACAGATTTGTTCATGGGACATCTAATAAATTAAATGAACTCTG

SEQ ID NO: 63_NEK7_H, N34132_H

CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGCGCCGCAG
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCTCTCGCCGCCGGCTCCTGCCCCAAGA
ACGGCTCCAGCTCCGATTCTCCGTGGGGGAGAACTGGGAGCCGCGGCCGCCGACGCTG
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCCGCCACACTATGGACAAGGACAGCCGTG
GGGCGGCCGCGACCACTACCACCACTGAGCACCCTTCTTCCGCCGAGCGTCATCTGCG
ACTCCAATGCCACTGCACTGGAGCTTCCCGCCTTCTCTTTCCCTGCCCCAGCCAGCA
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG
CCACCGCCACTTCCCAGGTAGCCAGCAGCCTCCAGCCGCTGCCGCCCTGGGGAACAGG
CCGTGCGGGGCCCTGCCCCCTCGACTGTCCCCAGCAGTACCAGCAAAGACCGCCAGTGT
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCCGCCGCGGAGAGTGGCAGCGGCG
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTTCTCAAGTTTGACATCGAAA
TCGGCAGAGGCTCCTTTAAGACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAG
TCGCCTGGTGTGAAGTGCAGGATCGAAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG
AAGAAGCTGAAATGTTAAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCTT
GGGAATCCACAGTAAAAGGAAAGAAGTGCAATTGTTTTGGTGACTGAACTTATGACGTCTG
GAACACTTAAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT
GGTGCCGTCAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG
GAGACCTCGGTCTGGCAACCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC
CAGAGTTCATGGCCCCTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA
ATGCTGCGCAGATCTACCGTCGCGTGACCACTGGGGTGAAGCCAGCCAGTTTGTGACAAAG
TAGCAATTCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA
GATATTCCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG
AAGATATTAAGAAATTAAAGGGAAAATACAAAGATAATGAAGCTATTGAGTTTTGTTTG
ATTTAGAGAGAGATGTCCCAGAAGATGTTGCACAAGAAATGGTAGAGTCTGGGTATGTCT
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAAACAAAAGCAGGAAGAGA
GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCAGACAGGAATCAAGCAGCTCC
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG
TAGAACCTGAAGAACCTGAGGCAGATCAACATCAACAACCTACAGTACCAGCAACCCAGTA
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTCACAGAAT
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCCAANNCATGAACAGGCACATT
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG
GGGTATATCCACCCCTCAAGTGTGTCAGCAGGGAATACAGCAGACAGCCCCCTCCTCAACAGA
CAGTGCAGTATTCATTTACAGACATCAACCTCCAGTGAGGCCACTATGCACAGCCAG
TGAGTCAGCCTCAAGCTCCACAAGTCTTGCCCTCAAGTATCAGCTGGAAAACAGAGTACTC
AGGGAGTCTCTCAGGTTGCTCCTGTCAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTGAGATGTTGCTTCAGGTATGA
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

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FIGURE 2YY

GGCATTACCGAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAT
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC
ATAATAGGAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGATCGTTTGTGGATC
AAGTGCGAGAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTCAGTGTGGAAC
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTCAGGTT
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA
TAGGCATTCTTACCAGTTCTTTAACTCAAGTTGTTTATTCTGCGGGAAGGCGGTTTATAG
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAGTTTTCCCCAGTGAAATAACAG
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT
CCCTTAGTCTACAACAGGCCTTTTCTGAACTTAGACGTGCCCAAATGACAGAAGGACCCA
ATACAGCACCTCCAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACTTCAGGTGGTCTCCCA
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTTCAAGTATCACAATACCTG
CAGTTGTCTCAATATCTACTACATCCCCGTCACTTCAAGTCCCCACATCCACATCTGAGA
TCGTTGTTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTTCAGCAACTTCAGCCTCTG
CAGGGGGCAGTACTGCTACCCCGAGTCTTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCCTTCATTCCCAA
GCACAGCTTCACAGCTGTCCATTAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG
AAACCGTGGTAGTTAGCGCACACTCACTAGATAAGACATCTCATAGCAGTACAACCTGGAT
TGGCTTTCTCCCTCTCTGCACCATCTTCTCTTCTCTCTCTGAGCAGGAGTGTCTAGTT
ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTCATTCCATCAGTGATAGCTTCTACTC
CTATTCTTCCCCAAGCAGCAGGACCTACTTCTACACCTTTATTACCCCAAGTACCTAGTA
TCCCACCTTGGTACAGCCTGTTGCCAATGTGCCTGCTGTACAGCAGACACTAATTCATA
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCTGAAGTAGATT
CTGATACACAACCCAAAGCTCCTGGAATTGATGACATAAAGACTCTAGAAGAAAAGCTGC
GGTCTCTGTTCACTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA
CCTCACTAGTCATAGAGAGCACTGTACACCAGGCATCCCACTACTGCTGTTGCACCAA
GCAAACCTCCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCCTAGGAA
CAGTTGCTTTGCCAGTTACACCAGTGGTCACACCTGGGCAAGTTTCTACCCAGTCAGCA
CTACTACATCAGGAGTGAAACCTGGAACCTGCTCCCTCCAAGCCACCTCTAATAAGGCTC
CGGTGCTGCCAGTGGGTACTGAACTTCCAGCAGGTACTCTACCCAGCGAGCAGCTGCCAC
CTTTTCCAGGACCTTCTCTAACCAGTCCCAGCAACCTCTAGAGGATCTTGATGTCTCAAT
TGAGAAGAACTTAGTCCAGAGATGATCACAGTGACTTCTGCGGTTGGTCTGTGTCCA
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTCTTCTCAAG
TCAAAGAAGGCCCTGTCTTAGCAACTAGTTTCCAGGAGTGGTGTCTTTTAAAGATGGGACGAT
TTCAGGTTTCTGTTGCAGCAGACGGTGCCAGAAAGAGGGTAAAAATAAGTCAGAAGATG
CAAAGTCTGTTTCAATTTGAATCCAGCACCTCAGAGTCCCTCAGTGCTATCAAGTAGTAGTC
CAGAGGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG
ATGTGCCAGAGAGTGCCCAAAAACCTACTGCCTCAGAGGCAAGTCAGACACTGGGCAGC
CTACCAAGGTTGGACGTTTTTCCAGGTGACAACTACAGCAAACAAAGTGGTCTGTTTCTCTG
TATCAAAAACCTGAGGACAAGATCACTGACACAAAGAAAGAGGACCAGTGGCATCTCCTC
CTTTTATGGAATTTGGAACAAGCTGTTCTTCTCTGCTGTGATACCAAAGAAAGAGAAGCCTG
AACTGTGAGAGCCTTCACATCTAAATGGGCCGTCTTCTGACCCGAGGCGCTTTTTTAA
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA
GCCTTCTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTTAACTCCTCTTACATGA
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC
GAGATAAACATCTCAAAGAGATTTCAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

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FIGURE 2ZZ

CTTTGTATACCAAACCTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC
TTTCAGGGGAGAAGACGACGACCCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT
CCTTGGGGGAATAAAAGCCCCCAGCTTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG
TCTTGCACCCCCCAGCAGACCCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAAATC
AGCTGTTACAGCCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTTCAGCCTTCACCA
GTGATGGTGCCATTTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTAAAG
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACTGAAGAATCTGG
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC
TCATTTGGGATTTGGAACCTTAGGCTTTAATATTAGGCTGAGATTTCTGGATGAAATTCT
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTCAGTTTTTTATCCA
TAATCTACTTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATTCCCACAGAG
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA
GATCAGTCTCTTCACAGGAAGAATGCACCTTGATTGGTAAGGAGGGCAAACCTAGCTAGCAT
TATTCGAACCTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT
CATCTCTTACATATCTGACCTTCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG
CATTTCAACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC
TCTCTCTGTTCTACCCTGTTTTTCCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTCTGAGTACGCCCTGCTT
GGCTCTTTGTGTGTAACACCTTTACTCCTTTCCTTGTCTTGTGTTTCTGCTGCTTGGATC
TGATGTTTCACGCAGTCCATTTTCATTTGTCTCTTTTTGTATATCATCTACTCAGTGGCT
TGGCTGAATTACTGTTACCCTCAGAAGTTTGGGCCCCCACAATTAATTATGATAAAAAATG
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACCTTCTGGTAGAAGTGCTTCTTCAT
GGATCTGTGACAGAGAGTGGATATGATATCTAGGCAATAGATTGCTGGGTCAATTAGAAT
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA
GGCGGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC
CCATCTCT

SEQ ID NO: 64_BCON3_H

GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT
GAAGCGCAGGCTGCGGGGCGCGGAGTCGGGAGGCCTGAGTGTTCTTCCAGCATGTCCGA
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC
AGCTCCTGGCCTGACATCAGTGTCACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAGAGTCGCCCTGTGGGCG
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA
ACGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTTCGTGCTGTGTTTGATAATCTGATTCA
ATTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAA
GGCCAGGGTCATTTTTATCACAGAATACATGTCTGCTGGGAGTCTGAAGCAATTTCTGAA
GAAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGACACA
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCT
GACCTGTGACACCATCTTCATCCAGCACACGGACTCATCAAGATTGGCTCTGTGGCTCC
TGACACTATCACAATCATGTGAAGACTTGTGAGAAGAGCAGAAGAATCTACACTTCTT
TGCACCAGAGTATGGAGAAGTCAATGTGACAACAGCAGTGGACATCTACTCCTTTGG
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTACAGGCAATGGAGAGTCCTCATATGT
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

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FIGURE 2AAA

CATTCAAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACCTCCTTGCGGCCCACTGCATTGTGGG
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAGGAGATGGATACTAG
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC
TCAGTCAACCAGCTCTGGAATTAGATAAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC
ACTTCTGCTGAAGTTGGAGGACAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTCAATTTTGCCAGGAA
CAGTACCCTCAACTCAGCCGCTGTCAACGCTCTCCTCTTAGAGCTCACTCGGGCCAGGCCC
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC
AGTATTACCCTGTGAAGCCCCTTCCCTCCTTTATTATTTCAGGAGGGCTGGGGGGGCTCCC
TGGTTCTGAGCATCATCCTTTCCCTCCCTCTCTTCTCCTCCCTCTGCACTTTGTTTACT
TGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCGCCTTCTAGTTGGGGGCTAGT
CGCTGATCTGCCGGCTCCCGCCAGCCTGTGTGGAAAGGAGGCCACGGGCACTAGGGGA
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGGAGAGAAAGGTGGTGCTGCAGTG
GTGGCCCTGGGGGGCCATTGATTGCTCCTCAGTTGCTGCTGTAATAAAAGTCTACTTTT
GCT

SEQ ID NO: 65_AA711829_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG
AAACGCTGGTGATACACAGATCCTCTCTGCCCTAAGCTACCTGCACCTCCTGTGACCTCCC
ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAAACGGACTCATCAAG
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTACGGGCAAT
GGCGAGTCCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC
TCATTACAGAGGGAGTTTATTCAAAAGTGCCCTGCAGTCTGAGCCTGCTCGGAGACCAACA
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC
AAGAACATGGATAACAGTGCTGTACTAGCTGAAATTCCCGCAGGGCCAGGACGAGAACCA
GTTCAAGACTTTGTAATCTCAGTCACCCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC
AGGAATGGGATCTACCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCCTGAGCCAGCT
GAAGTGGAGACACGAAAGGTGGTGCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC
TGTGACCTGATGCCAAATGAGAGCATCCCGACTTGGCAGCTGAGCTGGTGCAGCTGGGC
TTCATTAGTGAGGCTGATCAGAGCCGCCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTCACCGTCTCCTCGTAGAGC
TCACTTGAGCCAGGCCCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCTCCT
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTTAGGAGGGCTTTAGGG
GCTCCCTGGTTGAGTATCACCTGCCCCCTTCCCTCTCTTCTCCTCCCTCTGCACTTTGTT
TACTTGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGGC
TAGTAGCTGACCTGCTGCCTCCTGCCCTACTTGTGTGGACAGGAGGCCACGGGCACTGG
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA
GGGGTGGCCCCCGGGGGGGGCATTGCAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC
TTTTTGCT

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FIGURE 2BBB

SEQ ID NO: 66_AA099102_H

ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCTC
TCATCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTCACCGAGTGTGAGCCG
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGCCCCCTGGAGGCCGATGGCCAAGAG
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCCCACCTCTCCGGTCGCAAGCTGTCT
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC
TGCATCTGCCCCGTCCCTGCCCTACTCACCCGTACAGTCCCCGCAGTCTCGCCTCGGCTG
CCCCGGCGGCCGACAGTGGAGTCTCACCACGTCTCCATCACGGGTATGCAGGACTGTGTG
CAGCTGAATCAGTATACCCTGAAGGATGAAATTGGAAAGGGCTCCTATGGTGTCTGTCAG
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG
CTGATCCGGCAGGCCGCTTTTCCACGTGCGCCTCCACCCGAGGCACCCGGCCAGTCTCT
GGAGGCTGCATCCAGCCCAGGGGCCCCATTGAGCAGGTGTACCAGGAAATTGCCATCCTC
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCTGGATGACCCCAATGAG
GACCATCTGTACATGGTGTTCGAACCTGGTCAACCAAGGGCCCGTGATGGAAGTGCCCAAC
CTCAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT
GACGCGCTCCTCTCAAACCTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCTGCTCTCT
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA
TACTGCTTTGTCTTTGGCCAGTGGCCATTTCATGGACGAGCGGATCATGTGTTTACACAGT
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCCACATAGCTGAGGACTTGAAG
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGCCGGAAATC
AAGCTGCACCCCTGGGTACGAGGCATGGGGCGGAGCCGTTGCCGTGCGAGGATGAGAAC
TGCACGCTGGTGAAGTGACTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTGACGCGCTGGAACTTGCTCACCAAAAAA
CCAACCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT
CCAGGGCACCGACCCGCCCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC
TGCCTGGAAAGTTGCTGGGCCCCCGCCCCGCTCCCCCGCACGCATGCATCCACTGCGG
CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67_5R69_17_2_H

CCGGGATGTGAGCCTGGTGGTTGGCAGCTGGAGCCACGTCCGAGGGGGAAGTGTGCGCAGC
ATTCTCTGCAGGCATCACAGACCTGAGGCAGTGGCCTCCGAGGGCACTGGACAGAAACA
GCCATCCAAGTGGCTGAGTGGAGGGACCCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT
CCCTCAGGTAGGGATCGGGGCGCCTTGTGCGCGCCAGCCACGTGTGGCGTCCGGTACAGT
CAGCAGAGTGCAGGGTGCGGGCACCAGGAAAGGGGGCGCAGGGGAATCCCGCGGGCCTC
GCGTTTGCAAACCTTCTCGCCTGGGCAGGAGGCGGTCTGTTGGAAAGAAGGTGGAAGAGCGA
GCTTTTTTGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA
TGGAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCTCGGCCTGATCAAGC
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTTCAAGCAG
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG
TGAACAGGAAGCTGAGTGTCTGGAAGGAGCTCTCGCTGTTACTTCAGGTTGAGCAAC
GCATGCCGTGTTTCACCCATAAGCCAAGGAGCGTCTGGGCACAGGAAGATCAGCAGGATG
CAGACGAAGACAGGCGAGCTTTCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAACTTTGAGGCAGTGTAAAGT
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAACCTAGAAGTCATCAGTTTACTGGGAC

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FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC
CACAGGTTTGGGGATCCATTCATGGCTAGCCCAGGCTTCTGTCCATGGAATAACATGTGG
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT
ATGAATAGAATCAAAGCTTCAGTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAAA
TTTAAATGCCCCTCATTCAATTCATTCAACAAAACCTGTGAGTATCTGGTTTATGCCAGA
GGCCATGCAAAGAGGTAACATAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC
CAAGCTCTGGGTAAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG
GGTTAAGGCTGGAGGGACAGGCGGGATTTGAAGAGGAGGGAAAGGAAGTGGATGACACAT
TCTGTAACTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT
GGGCTGAGTCCATCAGAAGCCCCAGCCACCACCAGCTCTGGTTCATGTAGTAGAGCTTCC
CACTCACACATCACAATATGCCACCTCCCTTAGGACCCCTTCTCTGCTCATTGACTCT
TTTGTCTTCTTCTCTCGGGGGTGAGGTGAGATTTACCACCAAAATGCATGCAGGAGAT
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC
CATAAAAGTATTCAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA
TAAGGAGATCAAACCATGAAGAAATTCGAATCTCCAACATCCTGCGTATATTTGGGAT
TTGCATTGATGAAACAGTGACTCCGCCTCAATTCTCCATTGTCTGAGTACTGTGAACT
CGGGACCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGCAAGCGCATGGT
CCTAGTCTGGGGCAGCCGAGGCCTATACCGGCTACACCATTGAGAAGCACCTGAACT
CCACGGAAAAATCAGAAGCTCAAACCTCCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC
AGGATTTGAGTTGAGGAAAACACAGACTTCCATGAGTTTGGGAACCTACGAGAGAAAAGAC
AGACAGAGTCAAATCTACAGCATATCTCTCACCTCAGGAACTGGAAGATGTATTTTATCA
ATATGATGTAAAGTCTGAAATATACAGCTTTGGAATCGTCCTCTGGGAAATCGCCACTGG
AGATATCCCGTTTCAAGGTGAAGAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTTCTG
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGGCCCATGATCCCTCTGTGCGGCCCT
CTGTGGATGAAATCTTAAAGAACTCTCCACCTTTTCTAAGTAGTGATCAAAATCTAAA
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAACTGGACATCTCTCTCTCAT
ATCCTTCGGCATTGGGTTATCTATGGGTGCAAGGAGTGGGCACGCTTCTCTGTACAAAT
AGAAAAAGATTCCAGTCATACAGGACACATCCCACTCCAAATGATATTTCCAAAAACATA
CCTCTGACAGTAACCTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT
CTTGGAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATTT
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGAAGTGTAT
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA
TCAAGACCAGAAGAACCCTCAAGCAGATCCCAGCCCAAATTGCCCATTCACACAATCAG
GAGCTAAATAAATTACTGTTGTCTTTT

SEQ ID NO: 68_H85811_H

CGCCCCGGCCCCCTCCCCGGCGCCCGCCACGGGAGGCGGTGATGCGGGCGCGGGCGGCCT
CGGCTGCGCCGAGAGCGGAGACACAGGCTCAAGATGGCAGATTCCGACTGAGGCTGGGGG
GGCCGAGCTCGCGCGCGCTTTCCCGTCCCGTTGCCATGAACCGCGGACACCCCGGCC
CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTCTCCCTCACACCC
TTCAATCAAGTGCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAAGTGGG
ACATGACTGGGTACGGCTCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCAAGCCTACCTT
ACGAGCAGACCATCGTCTTCCCAGGAAGCACCGGGCACATCGTGGTCACTCAGCAAGCA

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FIGURE 2DDD

GCACCTTCTGTACCGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTCTGAAGCACTG
TGAGCCTCCTTGATACCTACCAAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTCAGAATAATGCAAGCG
GGGCCACTGTGCCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG
AGGTCTTAGAGTTCTTGCGCCGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAAACGGG
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCGACAAG
GTCAGATTGAAGTGAGCATCCTGCGCCGGTTGAGCACGGAGAGTGCCGATGACTATAACT
TCGTCCGGGCCTACGAATGCTTCCAGCACAAGAACCACACGTGCTTGGTCTTCGAGATGT
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCCTTGCCCCCTCAAAT
ACATTCGCCCAGTTCTCCAGCAGGTAGCCACAGCCCTGATGAAACTCAAAGCCTAGGTC
TTATCCACGCTGACCTCAAACCAGAGAACATCATGCTGGTGGATCCATCTAGACAACCAT
ACAGAGTCAAGGTCATCGACTTTGGTTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA
CCTACTTGCAGTCCAGATATTACAGGGCCCCCTGAGATCATCCTTGGTTTACCATTTTGTG
AGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGCAGAATTGTTCTGGGTTGGCCGT
TATATCCAGGAGATTTCGGAGTATGATCAGATTCCGTATATTTCAAAACACAGGGTTTGC
CTGCTGAATATTTTAAAGCGCCGGGACAAAGACAACCTAGGTTTTTCAACCGTGACACGG
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA
TTAAGTCAAAGAAGCAAGAAAGTACATTTTCAACTGTTTAGATGATATGGCCCAGGTGA
ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGGCGGGAGT
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG
AAACCCTGAACCATCCCTTTGTCACCATGACACACTTACTCGATTTTCCCCACAGCACAC
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC
TGACCATGACCTTTAAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA
TGGCTGCAGTGGCCCAGCGGAGCATGCCCTGCAGACAGGAACAGCCCAGATTTGTGCCC
GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAGG
CCTCTCCCTCTAAGCACGCTGGCTACTCGGTGCGAATGGAAAATGCAGTTCCCATCGTCA
CTCAAGCCCCAGGAGCTCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCCAGCAGGCTT
GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC
AGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGC
AGCCTGCACTATTGACCGGTTCATGTGACCCTTCCAGCAGCACAGCCCTTAAATGTGGGTG
TGGCCCACGTGATGCGGCAGCAGCCAACCAGCACCACTCCTCCCGGAAGAGTAAGCAGC
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCCTCTCAGGCCATCAGCT
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACAACCTCCCCGCTGTGCCATGGTGCACA
GTAGCCCGGCCTGCAGCACCTCGGTACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCA
CCCGGGAACGGCAGCGGCAGACAATTGTCAATTTCCCGACACTCCCAGCCCCACGGTCAGCG
TCATCACCATCAGCAGTGACACGGACGAGGAGGAGGAACAGAAACACGCCCCCACCAGCA
CTGTCTCCAAGCAAAAGAAAAACGTTCATCAGCTGTGTACAGTCCACGACTCCCCCTACT
CCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG
TGCCAGTCAACACCAGTCACCACTCGTCTCCTACAAGTCCAAGTCTCCAGCAACGTGA
CCTCCACCAGCGGTCACTCTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCACCATGG
CCCAGGCTCCGTACTCCTTCCCGCACAACAGCCCCAGCCACGGCACTGTGCACCCGCATC
TGGCTGCAGCCGCTGCGCGTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCACCTGGTGGCCTCGCAAGGCTCTG

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FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA
GCATGGGCCCCCGGGTCTGCCCTCGCCACCATCCACCCGAGTCAGTATCCAGCCCAAT
TTGCCACCAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCCAC
TGAGCCCCGCCAAGGTCAACCAGTACCCTTACATATAAACTGGAGGGGAGGGAGGGAG
GGAGGGAGGGAGAGAATGGCCCGAGGGAGGGAGGAGAGAAGGAGGGAGGGCGCTCCTGGGA
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG
GGCGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTCTGGGACACCAGTGAAACTTGAACC
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTAAAAGGAAGGGATTAAAGAG
GGTGGGAAATCTATGGTTTTTATTTTAAAAAAG

SEQ ID NO: 69_DYRK3_H

CGGGAGCGAAAGTGCCTGAGCTGCAGTGTCTGGTCGAGAGTACCCGTGGGAGCGTCGCG
CCGCGGAGGCAGCCGTCCCGGCGTAGGTGGCGTGGCCGACCCGACCCCCAACTGGCGCCT
CTCCCCGAGCGGGGTCCCGAGCTAGGAGATGGGAGGCACAGCTCGTGGGCCTGGGCGGAA
GGATGCGGGGCGCCTGGGGCCGGGCTCCCGCCCCAGCAGCGGAGTTGGGGGATGGTGTCT
TATGACACCTTCATGATGATAGATGAAACCAATGTCCCCCTGTTCAAATGTACTCTGC
AATCCTTCTGAACCACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA
GATCATACTCAGCACTTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA
TTTGGAACAGAAAATCCAATACTATTTCAGTCAGATGGCATCAGTGAATCTGAAAAATGC
TCTCCTACTGTTTCTCAGGGTAAAAGTTTCAGATTGCTTGAATACAGTAAAAATCCAACAGT
TCATCCAAGGCACCCAAAGTGGTGCCTCTGACTCCAGAACAAAGCCCTGAAGCAATATAAA
CACCACCTCACTGCCTATGAGAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTA
GGTCCAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT
GATGCAGATGGGGCCTATATTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG
CTGAAAATTATTGGCAAGGGGAGTTTGGGCAGGTGGCCAGGGTCTATGATCACAACTT
CGACAGTACGTGGCCCTAAAAATGGTGCGCAATGAGAAGCGCTTTCATCGTCAAGCAGCT
GAGGAGATCCGGATTTTGGAGCATCTTAAGAAACAGGATAAACTGGTAGTATGAACGTT
ATCCACATGCTGGAAAGTTTCACATTCCGGAACCATGTTTGCATGGCCTTTGAATTGCTG
AGCATAGACCTTTATGAGCTGATTAAAAAAATAAGTTTCAGGGTTTACCGTCCAGTTG
GTACGCAAGTTTGGCCAGTCCATCTTGCAATCTTTGGATGCCCTCCACAAAAATAAGATT
ATTCCTGCGATCTGAAGCCAGAAAACATTCTCCTGAAACACCACGGGCGCAGTTCAACC
AAGGTCATTGACTTTGGGTCCAGCTGTTTCGAGTACCAGAAGCTCTACACATATATCCAG
TCTCGGTTCTACAGAGCTCCAGAAATCATCTTAGGAAGCCGCTACAGCACACCAATTGAC
ATATGGAGTTTTTCGCTGCATCCTTGCAGAACTTTTAACAGGACAGCCTCTCTTCCCTGGA
GAGGATGAAGGAGACCAGTTGGCCTGCATGATGGAGCTTCTAGGGATGCCACCACCAAAA
CTTCTGGAGCAATCCAAACGTGCCAAGTACTTTATTAATTCCAAGGGCATACCCCGCTAC
TGCTCTGTGACTACCCAGGCAGATGGGAGGGTTGTGCTTGTGGGGGGTCTGCTCACGTAGG
GGTAAAAAGCGGGGTCCCCCAGGCAGCAAGAGACTGGGGGACAGCACTGAAAGGGTGTGAT
GACTACTTGTTTATAGAGTCTTTGAAAAGGTGTCTTCACTGGGACCCCTCTGCCCGCTTG
ACCCAGCTCAAGCATTAAGACACCCTTGGATTAGCAAGTCTGTCCCCAGACCTCTCACC
ACCATAGACAAGGTGTCAGGGAAACGGGTAGTTAATCCTGCAAGTGCTTTCCAGGGATTG
GGTTCTAAGCTGCCTCCAGTTGTTGGAATAGCCAATAAGCTTAAAGCTAACTTAATGTCA
GAAACCAATGGTAGTATACCCCTATGCAGTGTATTGCCAAAACCTGATTAGCTAGTGGACA
GAGATATGCCAGAGATGCATATGTGTATATTTTATGATCTTACAAACCTGCAAATGGA
AAAAATGCAAGCCCATTGGTGGATGTTTTTGTAGAGTAGACTTTTTTTAAACAAGACAA
AACATTTTTATATGATTATAAAGAATTCTTCAAGGGCTAATTACCTAACCAGCTTGTAT
TGGCCATCTGGAATATGCATTAAATGACTTTTTTATAGGTCA

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FIGURE 2FFF

SEQ ID NO: 70_AA589241_M_DYRK3_M

CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAACTTCTGGAGCAATCCAAGCGTG
CCAAGTACTTTTATTAACCTCAAAGGCTTGCCTCGATACTGCTCCGTATCTACCCAGACGG
ACGGGAGGGTGGTGCTTCTCGGGGGTTCGCTCAGCAGGGGTAAAAAGCGAGGCCCCGCCAG
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTCATAGAGTTTC
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCCGCTCAGCCCGCTCAAGCATTAAGAC
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC
GGGTAGTTAAACCCTACAAATGCTTTCCAGGGACTGGGTTCCAAGCTGCCTCCAGTCGTTG
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT
GTATTTTTTAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTAC
TGATGGATATGTTTTTGTAGACTTTTTTTTAAACAAGGCAGAACATTTTTATATGACTAT
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71_5R72_16_2_H

GTCGAGGCGCAGCGCTGCCATGGCTGGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGA
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA
CGGCGCGGACTTCCAAGACCTGCGGCCGACGCTTGCAGGACCGGTCAAAGAGCCCCCTGA
AATCAATTTAGTTTTGTACCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA
TTTGAGGGTTAAATGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAA
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGC
CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA
AATCCTGCATGAGATTCAAGAAAGGAAGAAGAGATAAAAAGAAGAGAAAAAAGGAAAGA
AATGGCTAAGCAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACTCTAA
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT
AGGAAATGGTAAACATCGGGCAAACCTCCTCAGGAAGGTCTAGGCGAGAAGTCAGTATTC
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAG
TCCTGATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACCTTGGAAA
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTGTATGAGTGGGT
CCTTCAGTGGCAGAAAAAATGGGTCCATTCTTACCAGTCAAGAAAAAGAGAAGATTGA
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAG
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTGAGGCCCTGA
TTATCTGCACAGCAATTCTGTGGTGCATAAGGTCTCTGAGTGCATCTAATGTCTTGGTGGA
TGCAGAAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG
CAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAA
AACGGGGAAGAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGA
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT
GAAACACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCCCTGAAGA
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCTAGCAACCGGCTACCCAGTGCTGC
CTTCTTTAGTGAGACACAGAGACAGTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCAAGGTGCAGAACAAAGTTGGACGGCTG
CTGCTACGCAGTGAAGCGCATCCCCATCAACCGGCCAGCCGGCAGTTCCGAGGATCAA
GGCGGAAGTGACACTGCTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC
CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCGGACTCCGGGCC

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FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA
CAGCGTAGAGGCCGCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC
GGGCGAGCGCTCGGCCAGTGCCCGTTTTCCCGCCACCGGCCCGGGCTCCAGCGATGACGA
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCAGTCCTTCTGCCTGCTTCAGA
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA
TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC
TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCAT
TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTTCGAGAGATTCTGGA
TGGATTAGCTTATATCCATGAGAAAGGAATGATTACCGGGATTGGAAGCCTGTCAACAT
TTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTTGGCGACAGACCATCT
AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC
TTCAGGTCACTTAAGTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG
AAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTT
TGAGATGTCCTATACCCCATGGTCACGGCTTCAGAAAGGATCTTGTCTCAACCAACT
CAGAGATCCCACTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA
GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAACCGGCCACAGCCACAGA
GCTGCTCAAGAGTGAGCTGCTGCCCCCACCACAGATGGAGGAGTCAGAGCTGCATGAAGT
GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGAT
CTTCTCGCAGCGCATCTCCCCTGCCATCGATTACACCTATGACAGCGACATACTGAAGGG
CAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCAT
CTTTAAAAGACATGGAGCTGTTCAAGTTGTGTACTCCACTACTGCTTCCCCGAAACAGACA
AATATATGAGCACAACGAAGCTGCCCTATTTCATGGACCACAGCGGGATGCTGGTGATGCT
TCCTTTTGACCTGCGGATCCCTTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTT
AAAACGATACTGCATAGAACGTGTGTTCAGGCCGCGCAAGTTAGATCGATTTTCATCCCAA
AGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCCCAC
TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG
AAATTACAGTATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGG
GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA
GCTGACGAGGAGAGAAGTGGAAGCTAAATTTGTAATCTGTCTTTGTCTTCTAATAGTCT
GTGTGCACTCTACAAGTTTATTGAACAGAAGGGAGATTGCAAGATCTTATGCCAACAAAT
AAATTCAATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAGA
CCTAGAGGAGGTTGTTGGACTGTTGAAGAACTCGGCATCAAGTTACAGGTCTTGATCAA
TTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT
CATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT
GCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGT
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCTCTCAACATGGAGGAATCTGTTACAAT
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAA
CCTAACCCAGAAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCA
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTTCGAGAAGGAAGGCAGACAGA
GAAGCGTGTGCTGGAGACTGAACTTGTGGACCATGTACTGCAGAAACTGAGGACTAAAGT
CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAAGTGCAAAATCTGAAGGG
GTCATTTTCTAATGCTTCAGGTTTGTGTTGAAATCCATGGAGCAACAGTGGTTCCCATTTGT
GAGTGTGCTAGCCCCGGAGAAGCTGTACGCCAGCACTAGGAGGCGCTATGAAACTCAGGT
ACAAACTCGACTTCAGACCTCCCTTGCCAACCTACATCAGAAAAGCAGTGAAATTGAAAT
TCTGGCTGTGGATCTACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGC
TGATGAACAGGCATTTAACACAACGTGAAGCAGCTGCTGTACGCCTGCCAAAGCAAAG
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGT
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCTAAAGAAC
TGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT

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FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA
TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG
CCT

SEQ ID NO: 73_R43524_H, HRI_H

ATGCTGGGGGGCAACTCCGGGGTCCGCAAGCGCAAGAGGAGGGCGACGGGGCTGGGGCT
GTGGCTGCGCCGCCGGCCATCGACTTTCCCGCCGAGGGCCCGACCCCGAATATGACGAA
TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCCTACAACAGCCAACCTTCCCT
TTTGAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT
GAACCAAACCACTTCGTTCAAGACAGGTGTTAAGCTACTTTGCCAGACGTTTATCAAA
ATGGGGCTGTTGTCTTCTTTCACTTGAGTGACGAGTTTAGCTCATTGAGACTACATCAC
AACAGAGCTATTACACACTTAATGAGGTCTGCTAAAGAGAGAGTTTCGTCAGGATCCTTGT
GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAACT
TCACGTTACTTAAATGAATTTGAAGAACTTGTCATCTTAGGAAAAGGTGGATACGGAAGA
GTATAACAAGGTCAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATT
AAGGGTGCAACTAAAACAGTTTGCATGAAGGTCTACGGGAAGTGAAGGTGCTGGCAGGT
CTTCAGCACCCCAATATTGTTGGCTATCACACCGCGTGGATAGAACATGTTTCATGTGATT
CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG
GAAGAGGACAGAGAGCAATGTGGTGTAAAATGATGAAAGTAGCAGCTCATCCATTATC
TTTGCTGAGCCCCACCCAGAAAAGAAAACGCTTTGGAGAATCTGACACTGAAAATCAG
AATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAAGTTGAG
TCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTTTGTCTGCCAGTTCAATTGTGGAA
CAGCAGCTGCCACTCAGGCGTAATTTCCACCTAGAGGAGAGTTTCACATCCACCGAAGAA
TCTTCCGAAGAAAATGTCAACTTTTTGGGTGAGACAGAGGCACAGTACCACCTGATGCTG
CACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAG
CGGGGCCGGGAGTATGTGGACGAGTCTGCCTGTCTTATGTTATGGCCAATGTTGCAACA
AAAATTTTTCAAGAATTGGTAGAAGGTGTGTTTTACATACATAACATGGGAATTGTGCAC
CGAGATCTGAAGCCAAGAAATATTTTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGA
GACTTTGGTCTGGCCTGCACAGACATCCTACAGAAGAACACAGACTGGACCAACAGAAAC
GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAA
CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCTCTG
CTAGAGCTCTTTCAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAAGTTCTAACAGGTTTA
AGAACTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC
CAGCACTTAACGAGAAGGAACTCATCGCAGAGACCATCTGCCATTAGCTGCTGCAGAGT
GAAGTTTCCAAAATTCTGGAAATGTTAACCTCACCCTACAGATGAAGATAATAGAGCAA
GAAAAGAAATTGCAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTG
AGGGATGACGGAAAGGATGGGGGCGTGGGATGA

SEQ ID NO: 74_17000057519457_H

CACAAGAGCCCTTCTGTCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT
AACCACCTTACAGGCCGGAAGTGTCCGGGGTGGACGCATTTCGGGTAGCCGAAGAAGTCCCA
GGATTGCCGAAGAAGTCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAG
AGACAGCTGATCGGTGAGCTGTTGCGCCGAGCAGTCATGGCGGCGCCAGAGCTACTA
CGCCGGCCGATGGCGAGGAGCCCGCCCGGAGGCTGAGGCTCTGGCCGAGCCCGGGGAGC
GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGT
TCCGTGGCCGCTTCCAGGGCCGCGCGGCTGATCAAGCACCGCTTCCCCAAGGGGCTACC
GGCACCCGGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGCAGGAGCCCGGGCGC
TCCTCCGCTGTGCGCCGCTGGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTT
CCAAGTCTTATATATGGAAGAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGT
CCACTATGGAGACTGAAAAAATCCCCAGGGTCTCTCCAAGTTAGCCAAGACAATTGGGC

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FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTCATGGTGATCTCACCACCTCCAACA
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT
TCATTTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC
TCAGTACCCATCCCAACACTGAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCT
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG
ATATTTTAAAGTGGTATGTGATCGTGTCTATTATCATCTGCACCTTCACTCAAGAGCTTACT
ATGTGTCTAAGTCATGTTCTAGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTT
CTCCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA
GAACATTATTCTCTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC
GCTGAGCTTACTGGCCCTCTAACCAGTGTTTTTTTTTTGTTGTTGTTGTGTACATGTTAT
ATTTATTTTGAAACCAGTTTAAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA
CAGCATGGAAAAATATCAGTGTATTGTTTTATGAAACTTTCACGTGTATATATAGACCAAG
GATATGTGCTGAGTTTGTATGTCAAATATATTTCTCTTTCAGGGTCATGATCAAAAAATG
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC
TGAAATTCATGTTAAACATGTTTTTATTTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA
AGACAAGTGATTGATCTAAAGTTCCTTTTAAAGTTTATACCGCTAAACAAACTGAGTTGAT
TTCTATCACAGGCAGTAAGTAGGTAGAGCAAAAAATGGTGAAGTGAAGTGTGAAGACTGAA
GTTTGATGAAGTCTGGTTTAAAGGCACAGGTAAACTGAGTGTGGATGCAAAAGTACCAGGA
GCTAGCTTTTAACTTGCCAGCCTCAGTTTCTTTTCTTAGAAGAAGCTATGTTTGGGTG
GGAAGGGAAGAGAGGGATAAGAAAATACCTTTCTTCTTGTAAACTCCAATCAACAAACA
TATTTTGAGTGCCTTTTGTGTTCTTGGCACCCCTGTTGGGTATTGGGTACTTGGCACCCCT
GTTGGGTATTGGGTACAATGGTGAGCCAGACAGACACAGCGCCTGTCTTTTGTAAAGAAT
ATTTATTTTTATAAAAAAGTATAAAGTATACAGTGGGATGTTTTGATATACATTATGAAA
TGATTGCTACAGCTGAGCTAATTAACACCCATCACCTCACATAGTTACTGTCTTGTCTTCT
TAATATGGACATTTGCAGCTATGAATTTCCCTCTGCACACTGTTGTATCACACACTCTC
AGTTTTGGTATTTTGTGTTTTTGTTTTTTCAATTCATCTCAAAGTATTTTCTAATTTCCCTTG
TGATTTCTTCTTTGACCCCTTGATTGTTTAGAAATCTGTTAATTTCCACACATTTGTAA
TGTTCCAATTTTCTTTTGTATTGTCAGCTTCAATTCATTGTGTTTCAAGATGATACAG
TCAGTGCCTGTTCTTATGAAGCAACATTCTATAATAGTAGGACCAGTACCCTGTCTGTT
TCATTACCCACAGTCAGCATGCCCAAGTGCCAGCATGGGGCGGATGGCCAGGAATGAG
TGAAACTTCCCTTCTTGGGTAGTTGTGACTAGTAGAGAGGAAAAATAATATAATTGCCT
GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTATATTGGATCTAAATAACTCTTA
AGTTAGGCATTATCCCCATTTTATAGATGGAGAAACTGGCCCCAAAGGTGGGAAGTTGT
CCAAGACGTCACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA
CTGACAAATGAGATATGGGATATGGTGCATCTTTACAGTACTATAATAAGTATTGGCGTA
TAACATTATTTTCAAGGAAGTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT
TCCCAACATGAATGAGATGCCTCATTCTCAGTTTCTCAGGTGTACTATAAGGCTAGTA
CCTGCTTTGTTGGGGTATGGTTGGCTCGTGTGCATTAAAGTCAACAAATCCCTAGT

SEQ ID NO: 75_AA013524_M

CTGGTGCAGCAGGGCGCCGAGGCGCGCGTTTTCCGTGGCCGCTTCCAGGGCCGCGCGGCC
GTGGTGAAGCACCCTTCCCGAAGAGTTACCGGCACCCGGAGCTGGAGGCGCGGCTCGGC
CGTCGGCGGACGGTGCAGGAGGCGCGCGCGCTGCTCCGCTGCCGCCGTGCGGGGATAGCT
GCCCCAGTCGTCTTCTTTGTGGACTATGCGTCTAACTGCTTATATATGGAAGAAATCGAA
GACTCGGTGACTGTTTGGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG
TGCCCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC
CTCATTACGGGGACCTCACCACCTCCAACATGCTCCTGAGGCGGCCCTGGCGCAGCTG
CACATCGTGCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

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FIGURE 2JJJ

GTCGACCTCTATGTCTGAGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG
TTTGAAGCCTTTCTGAAGAGTTACGGGGCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCCGGTAGTGAGCTGT
GGTGAACCTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG
GGTTGTTAAGTGGTCTGTGATCGTGCTGGGCCACCACCATCCATGGCTCACTGTTCTCAG
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGGAAGAGGTTATAAGCCACCATACCT
GACTTTGCACTGATTCTGTCAGAAAC

SEQ ID NO: 76_17000139801197_H, IRAKM_H

ATGGCGGGGAAGTGTGGGGCCCGCGCGCGCTGTGGCGGCACACGCTGCTGTTGACCTG
CCGCCCGCGCTGCTCGGAGAGCTCTGCGCTGTTCTGGACAGCTGCGACGGCGCGCTGGGC
TGGCGCGGCCTGGCAGAGAGACTTTCAAGCAGCTGGCTGGATGTTTCGTATATTGAAAAG
TATGTAGACCAAGGTAAAAGTGAACAAGAGAATTACTTTGGTCTGGGCACAGAAAAAC
AAGACCATCGGTGACCTTTTACAGGTCTCCAGGAGATGGGACATCGTCCGAGCTATTCAT
TTAATTACAACTATGGAGCAGTGTGAGTCCTTCAGAGAAGAGTTATCAGGAAGGTGGA
TTTCCAAATATATTATTCAAGGAAACAGCCAATGTCAACGTTGGATAATGTTCTTATTCCT
GAACATAATGAAAAAGGAGTACTGCTTAAATCTTCCATCAGCTTTCAAAATATCATAGAA
GGAAGTAGAAATTTCCACAAAGACTTCCTAATTGGAGAAGGAGAGATTTTTGAGGTATAC
AGAGTGGAGATTCAAAACCTAACATATGCTGTCAAATTAATTTAAACAGGAGAAAAAATG
CAGTGTAAGAAGCATTGGAAGAGGTTTTTATCTGAGCTTGAAGTTTTACTACTGTTTCAT
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT
TATCCATACATGAGAAATGGAACACTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCC
CCACTCCCTTGGCACATTGGAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC
CTGCACAACGTTCAACCATGCTCGGTATCTGTGGCAGTATATCAAGTGCAAACATCCTT
TTGGATGATCAGTTTCAACCCAACTAACTGATTTTGCCATGGCACACTTCCGGTCCCAC
CTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTAC
ATGCCAGAAGAGTACATCAGACAGGGGAACTTTCCATTAAACAGATGTCTACAGCTTT
GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTAGATGATCCAAACAT
ATCCAGCTGCGGGATCTCCTTAGAGAATTGATGGAGAAGAGAGGCCTGGATTCTGTCTC
TCATTTCTAGATAAGAAAGTGCCTCCCTGCCCTCGGAATTTCTCTGCCAAGCTCTTCTGT
TTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTTA
AATACTCTTGAAAGTACTCAAGCCAGCTTGATTTTGCTGAAGATCCTCCACATCACTA
AAGTCCTTCAGGTGTCCTTCTCCTTATTCTGGAAGATGTACCAAGTATTCAGTGGAA
GATGATGAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCCTGAGGATAGACAGA
ATGACTCAGAAAACCTCTTTTGAATGCAGCCAGTCTGAGGTTATGTTTCTGAGCTTGGAC
AAAAAGCCAGAGAGCAAGAGAAATGAGGAAGCTTGCAACATGCCAGTCTTCTTGTGAA
GAAAGTTGGTTCCCAAAGTATATAGTTCCATCCCAGGACTTAAGGCCCTATAAGGTAAAT
ATAGATCCTTCTTCAGAAGCTCCAGGGCATTCTTGCAAGGAGCAGGCCAGTGAGAGCAGC
TGTTCTCCAAATTTCTCTGGGATGAATATGAACAGTACAAAAAAGAATAA

SEQ ID NO: 77_AA840598_M IRAKM_M

ATGTGGAAGAGATTTTATCAGAACTGGAAGTTCTACTCCTGTTCCGTCACCCCCACATA
CTAGAGCTGGCTGCATATTTACGGAGACTGAGAACTTTGTCTGGTTTATCCCTATATG
AGCAACGGGACGCTTTTCGACAGATTACAGTGACAAATGGCACAACCCCGCTTCTCTGG
CACGTTCCAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGACAAACACT
CAGCCGTGCGCCGTCATCTGTGGCAACGTTTCCAGTGCAAAACATACTCTTGATGACCAG
CTCCAACCCAACTAACGGATTTTGCTGCAGCGCACTTCCGACCCAACTTAGAGCAGCAG
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

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FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACTGATGTCTACAGCTTCGGAATCGTGATC
ATGGAGGTTCTAACGGGCTGCAAAGTGGTGCTGGATGACCCGAAACAGTTTCAGCTGCGG
GACCTCCTCATGGAAGTGTGGAGAAAAGAGGCCTAGACTCCTGCCTGTCTTCTTAGAC
AGGAAGATAACCACCTGTCTCGGAAGTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG
TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCTGTCTCTGAGAG
AGCACCCAGCCTAGCTTGTATTTTGAGAAGACCTCCACGTCCTTGAAGTCCTTCAGG
TGTCTTCTCCACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAAC
CAGAATAACCATTTCAGTACCTCCCAAGGAAGTTTTGGGGACAGATAGAGTGACTCAGAAA
ACCCCTTTGAATGCAGCCAGTCTGAGGTCACTTTCTAGGCTTGGACCGAAACAGAGGG
AACAGGGGAAGTGAAGCGGATTGCAACGTGCCAGTTCTTCTCATGAGGAATGCTGGTCC
CCAGAGCTTGTGGCGCCATCCAGGACTTAAGTCTTACTGTGATCAGTTTGGGCTCGTCT
TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG
CTCTTTTGCAGTGAGCATGAACAGTCCAAAAAGCAGTGAATCCACCAGAAGATCAAGCAA
AAAATAAAAGCAAACGTCAGTGAAGGCACTGAGCAAATAGCATCCCCGTGAAAAGACACG
AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCAACTGATGGAGAATTTGAATGGTGCAG
ATTAGCAGCAAGGAAGTCTATTCTTCTCCAAACAGAATAATTTCAAGAGATGCTTTAT
TCAAGTGACCGCCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC
AAGATTCCGGGTTCTGACAACCAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT
AAGTCTCTCACTCTCTCTCATCATCCGAGTGAGATCTTGGTATAGGTGAACAGAGAACCA
CCCACCTTCCAGAACCAGAACCACCTTCTCCCCAAGCCAGCAGTCAGTCACTCACCATCA
GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC
CTACGTCTTTATAAAACCCAGGTCTTCAGGGCCCAACCCCTTTCTTTTCCATCCTTGCT
CAGAGGCAGCCTTTTGTATACATTCCCTGACCCCAACCCCAATTATATCTCTCATATGATA
TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTGAGATCATTTGCACAAGAACA
AGCGAATACACAACAACAAGCCCAACCATCATACCACCGGCACTTAATGCTAGTCTTTC
TGCTAGGGATACTGACAGTCTATTTGCTTCCCATGGTCATAGGGAAGTTGCTCAAATGCA
AAGGTTGTAGGGAATGTCTAATTTGTAAATGGCGTCGGGTGCCTTTGGAAGGAATTGTGT
TTTTACAGCCAGTTGCTACTCTTGTATTCGCTGGTTAACCGGTCTGTCCGGAAGTGAGC
CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCCAGTCCAAAGTCTGCT
TCTCTGTATTTAAATTCTTAGAAGAGTTGCCGTGTGGCATTCCAATTGTTATATAAAAAA
TTATATTAAAGAATTCCAGCACT

SEQ ID NO: 78_AA088547_H

ATGGCGAGTGCGGTGAGGGGGTTCGAGGCCGTCGGCCCCGGCTGGGGCTCCAGCTCCAGTTC
GCGGCGCTGCTGCTCGGGACGCTGAGTCCACAGGTTTCATACTCTCAGGCCAGAGAACCTC
CTGCTGGTGTCCACCTTGGATGGAAGTCTCCACGCACTAAGCAAGCAGACAGGGGACCTG
AAGTGGACTCTGAGGGATGATCCCGTCATCGAAGGACCAATGTACGTACAGAAATGGCC
TTTCTCTCTGACCCAGCAGATGGCAGCCTGTACATCTTGGGGACCCAAAAACAACAGGGA
TTAATGAAACTGCCATTCACCATCCCTGAGCTGGTTTCATGCCTCTCCCTGCCGCAGCTCT
GATGGGGTCTTCTACACAGGCCGGAAGCAGGATGCCTGGTTTGTGGTGGACCCTGAGTCA
GGGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCCGCCTCTACATTGGC
CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC
ACCTACCGCCGCTACTCAGCGCCCCCATGGATGGCTCACCTGGGAAATACATGAGCCAC
CTGGCGTCTGCGGGATGGGCCTGCTGCTCACTGTGGACCCAGGAAGCGGGACGGTGTCTG
TGGACACAGGACCTGGGCGTGCCTGTGATGGGCGTCTACACCTGGCACCAGGACGGCCTG
CGCCAGCTGCCGCATCTCACGCTGGCTCGAGACACTCTGCATTTCTCGCCCTCCGCTGG
GGCCACATCCGACTGCCCTGCCTCAGGCCCCCGGGACACAGCCACCCCTTCTCTACCTTG
GACACCCAGCTGCTAATGACGCTGTATGTGGGAAGGATGAACTGGCTTCTATGTCTCT
AAAGCACTGGTCCACACAGGAGTGGCCCTGGTGCCTCGTGGACTGACCCTGGCCCCCGCA
GATGGCCCCACACAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

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FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT
GGACACCACGAGCTACCCCCAGTCTGCACACCACCATGCTGAGGGTCCATCCCACCCTG
GGGAGTGGAAGTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG
GAGCTATTGAGCCTGAGCCGAGAGAACTTTGGGACTCCGAGCTGCATCCAGAAGAAAA
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG
ACCCCCCTGGCACCTGCAGACTTTGCTCACATCTCCAGGATGCCAGTCCCTGCACTCG
GGGGCCAGCCGGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCCAGCCACTC
GACGACCCTGAAGCTGAGCAACTCACCGTAGTGGGGAAGATTTCTTCAATCCCAAGGAC
GTGCTGGGCCCGCGGGCAGGCGGGACTTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCCTGGTTCGGCGGGAAGTTCAACTG
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCGAGCGGGGACCC
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCTCCTTGCAGGAGTACGTAGAAAAAC
CCGGACCTGGATCGCGGGGGTCTGGAGCCCGAGGTCTGTGCTGCAGCAGCTGATGTCTGGC
CTGGCCACCTGCACTCTTTACACATAGTGACCCGGGACCTGAAGCCAGGAAATATTCTC
ATCACCGGGCCTGACAGCCAGGGCCTGGGCAGAGTGGTGTCTCAGACTTCGGCCTCTGC
AAGAAGCTGCCTGCTGGCCGCTGTAGCTTCAGCCTCCACTCCGGCATCCCCGGCACGGAA
GGCTGGATGGCGCCCGAGCTTCTGCAGCTCCTGCCACCAGACAGTCTTACCAGCGCTGTG
GACATCTTCTCTGCAGGCTGCGTGTCTACTACGTGCTTTCTGGTGGCAGCCACCCCTTT
GGAGACAGTCTTTATCGCCAGGCAAACATCCTCACAGGGGCTCCCTGTCTGGCTCACCTG
GAGGAAGAGGTCCACGACAAGGTGGTTGCCCCGGACCTGGTTGGAGCCATGTTGAGCCCA
CTGCCGAGCCACGCCCCCTCTGCCCCCAGGTGCTGGCCCACCCCTTCTTTTGGAGCAGA
GCCAAGCAACTCCAGTTCTTCCAGGACGTCACTGACTGGCTGGAGAAGGAGTCCGAGCAG
GAGCCCCCTGGTGAGGGCACTGGAGGCGGGAGGCTGCGCAGTGGTCCGGGACAACCTGGCAC
GAGCACATCTCCATGCCGCTGCAGACAGATCTGAGAAAGTTCCGGTCCCTATAAGGGGACA
TCAGTGGGAGACCTGCTCCGTGCTGTGAGGAACAAGAAGCACCCTACAGGGAGCTCCCA
GTTGAGGTGCGACAGGCACTCGGCCAAGTCCCTGATGGCTTCGTCCAGTACTTCACAAAC
CGCTTCCACGGCTGCTCCTCCACACGCACCGAGCCATGAGGAGCTGCGCCTCTGAGAGC
CTCTTCTGCCCCCTACTACCCGCCAGACTCAGAGGCCAGGAGGCCATGCCCTGGGGCCACA
GGGAGGTGA

SEQ ID NO: 79_HGP_6644466

GGAGGGTTTCAATTGCAACGGCAGCTGCCGGGCGTATGTGTTGGTGCTAGAGGCAGCTGC
AGGGTCTCGCTGGGGGCGCTCGGGACCAATTTTGAAGAGGTACTTGGCCACGACTTATT
TTCACCTCCGACCTTTCCTTCCAGGCGGTGAGACTCTGGACTGAGAGTGGCTTTCACAAAT
GGAAGGGATCAGTAATTTCAAGACACCAAGCAAATTATCAGAAAAAAGAAATCTGTATT
ATGTTCAACTCCAATAATAATATCCCGGCCTCTCCGTTTATGCAGAAGCTTGGCTTTGG
TACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTG
GGCTGTAAAAAAGATTAATCCTATATGTAATGATCATTATCGAAGTGTGTATCAAAGAG
ACTAATGGATGAAGCTAAGATTTTGAAGAGCCTTCATCATCCAACATTGTTGGTTATCG
TGCTTTTACTGAAGCCAATGATGGCAGTCTGTGTCTTGCTATGGAATATGGAGGTGAAAA
GTCTCTAAATGACTTAATAGAAGAACGATATAAAGCCAGCCAAGATCCTTTTCCAGCAGC
CATAATTTTAAAAGTTGCTTTGAATATGGCAAGAGGGTTAAAGTATCTGCACCAAGAAAA
GAAACTGCTTCATGGAGACATAAAGTCTTCAAATGTTGTAATTAAAGGCGATTTTGAAC
AATTAATCTGTGATGTAGGAGTCTCTCTACCACTGGATGAAAATATGACTGTGACTGA
CCCTGAGGCTTGTTACATTGGCACAGAGCCATGGAAACCCAAAGAAGCTGTGGAGGAGAA
TGGTGTATTACTGACAAGGCAGACATATTTGCCTTTGGCCTTACTTTGTGGGAAATGAT
GACTTTATCGATTCCACACATTAATCTTTCAAATGATGATGATGATGAAGATAAAACTTT
TGATGAAAGTGATTTTGATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT
TAATATGGAAGAACTGGATGAATCATACCAGAAAGTAATTGAACTCTTCTCTGTATGCAC

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FIGURE 2MMM

TAATGAAGACCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA
TGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCGTAAATAACTGTTTATTCCAAAATA
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG
TTTCTTGTTAACATATGGATAACTATTTCTAATATGAAATATGCTTATATTGGCTATAAG
CACTTGGGAATTGTACTGGGTTTTCTGTAAAGTTTGTAGAACTAGCTACATAAGTACTTTG
ATACTGCTCATGCTGACTTAAAACACTAGCAGTAAAACGCTGTAACTGTAACATTAAAT
TGAATGACCATTACTTTTATTAATGATCTTTCTTAAATATTCTATATTTTAATGGATCTA
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAAACACTGAACC
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA
GTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGGATCTCCTC
AGATCTTTGGTTTTTGTCTTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAAATTTA
TTAATTTGTACCTTAAGCATTTCCAGCTGTGTAAAAACAATAAACTCAAATAGGATGA
TAAAGAATAAAGGACACTTTGGGTACCAGAAGGTGTCTCAGCATTATTTTATACTTC

SEQ ID NO: 80_AA449542_M

ATCTCCAAGAGGGTTGTCTCATTCTCCTTGGGCCGTGAAAAAGATAAGTCTTTTATGCGA
TGATCATTATCGAACTGTGTATCAGAAGAGACTAACTGATGAAGCTAAGATTTTAAAAA
CCTTAATCACCCAAACATTATAGGATATCGTGCTTTTACTGAAGCCAGTGATGGTAGTCT
GTGCCTTGCTATGGAGTATGGAGGTGAAAAGTCTCTGAATGACTTAATAGAAGAGCGGAA
CAAAGACAGTGGAAAGTCCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC
AAATGTTGTAATTAAAGGTGATTTTGAACAATTAAAATCTGTGATGTAGGAGTCTCTCT
GCCATTGGATGAAAATATGACTGTGACTGATCCTGAGGCCTGTTATATTGGTACTGAGCC
ATGGAACCCCAAGGAAGCGTTGGAAGAAAATGGCATCATTACTGACAAGGCAGATGTGTT
TGCTTTTGGCCTTACTCTGTGGGAAATGATGACTTTATGTATTCCACACGTCAATCTTCC
AGATGATGATGTTGATGAAGATGCAACCTTTGATGAGAGTGACTTCGATGATGAAGCATA
TTATGCAGCTCTGGGGACAAGGCCATCCATCAACATGGAAGAGCTGGATGACTCCTACCA
GAAGGCCATTGAACTCTTCTGTGTGTGCACTAATGAGGATCCTAAAGATCGCCCGTCTGC
TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA
TTAAGTTGTATGGGAAGTGTAACTAGATATATGTAGTTAATATAACTTATGGTAGCTAG
ATTCTAGAAGTAGCTTTAACACTAGTGACCCCTGTCTAAGATGACTTAAGAATCAAGGGA
CCATTGCTTTGTTACAGATCTTTTATGATATCTTGCTTCTTTAGTGGGTTACTAAAAAT
TTCACTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTGAGTCTTCCAGCTGGC
CTGTGAGCCCATGCGCCCTGGGACTTGAGAAGAGTTTATAAACGTAGCTCCTAGGGTGTCT
TTGCCTCTCTACACTTAGCTTCTAATTTATTACTTTGTTTCTACTGATTGTGTCTTAAGT
CTTTTAAAAATAAATGTAAGAATAAACAATAAAAGACAGTTTATAGTACCAGG

SEQ ID NO: 81_5R57_10_2_M TESK2_M

GCTGCTGGACAGTGACTTGTATTTACCGTGGACTGTGAGAGTGAACTGGCCTATGGCAT
AGCAGTGGGCCTCAGCTACCTTCAAGGCATTTTCCATCGGGACCTCACATCAAA
GGTGTGAAGGCTTTGCTTTC

SEQ ID NO: 82_AA232253_H

ATGTCGTCTCTCGGTGCCTCCTTTGTGCAAATTAAATTTGATGACTTGCAGTTTTTTTGAA
AACTGCGGTGGAGGAAGTTTTGGGAGTGTATCGAGCCAAATGGATATCACAGGACAAG
GAGGTGGCTGTAAAGAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTC
AGTCACAGAAACATCATCCAGTTTTATGGAGTAATTCTTGAACCTCCCACTATGGCATT
GTCACAGAAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAG
GAGATGGATATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTAT
TTACATATGGAGGCTCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTT

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FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT
ACAACACACATGTCCTTGGTTGGAACCTTTCCCATGGATGGCTCCAGAAGTTATCCAGAGT
CTCCCTGTGTGAGAACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTA
ACAAGGGAGGTCCCCTTTAAAGGTTTGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAA
AAAAACGAGAGATTAACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACAT
CAGTGTGGGAAGCTGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCATCCTG
GAGTCCATGTCAAATGACACGAGCCTTCCTGACAAGTGTAACCTATTCTACACAACAAG
GCGGAGTGGAGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGAT
CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA
AAGCTGACAGAGCAGTCCAACACCCCGCTGCTGCCTTCCTTTGAGATTGGTGCATGGACG
GAAGACGATGTGTATTGGTGGGTTTCAGCAGCTCGTCAGAAAAGGTGACTCTTCAGCAGAG
ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG
CTGGAGGAAGAAGACCTGAAAGACATGGGCATTGTCTCCAAGGGGCATATCATTCACCTTC
AAGTCAGCCATTGAGAAATTAACCCATGATTACATAAATTTGTTTCACTTCCCACCACTA
ATTAAGGACTCAGGAGGTGAACCTGAAGAAAATGAGGAAAAAATAGTGAACCTGGAACCTG
GTTTTTGGTTTTTCACTTGAAACCAGGAAGTGGCCACAGGATTGTAAGTGGAAAATGTAT
ATGGAGATGGATGGGGATGAAATTGCAATAACCTACATAAAAGATGTGACATTCAACACT
AACCTACCTGATGCGGAGATTTTAAAGATGACAAAGCCACCATTGTGAATGGAGAAGTGG
ATTGTAGGAATAGCAAAAAGTCAGACTGTGGAGTGCCTGTGCATATGAGAGTGTGTT
AGAATCCAAAAAGCACTAAACATGTCCATTTGATTCACTGGAGTAGAACAAAACCTCAG
GATGAAGTGAAAGCAGTCCAACCTTGCCATTGACATTTATTCACCAATTGAGATGGCAAC
CCTGGAAGCAGGTCCGACTCAAGTGCTGATTGCCAGTGGTTAGATACTCTGAGGATGCGG
CAGATTGCATCCAACACTTCTTTACAGCGTTCCAGAGCAATCCTATTCTGGGGTCACCG
TTCTTCTCACACTTTGATGGCCAGGATTCTACGCTGCTGCTGTGAGACGGCCCCAGGTG
CCCATTAAGTATCAACAGATTACACCTGTGAACCAAGTCCAGAAGCTCGTCTCCTACTCAG
TATGGACTGACCAAAAACCTTCTTCTTCTTACATCTCAACTCTAGGGACAGTGGCTTTTCC
AGTGGCAATACTGACACCTCTTCAGAGAGGGGTGATACTCAGACAGAAGCAGGAACAAA
TATGGACGTGGTAGTATATCACTCAATTCTTCTCTAGAGGAAGATACAGTGGAAAGAGT
CAGCATTCCACTCCATCAAGAGGAAGATACCCTGGAAAGTTCTACAGGGTTTCTCAGTCA
GCACTCAATCCTCACCAGTCGCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC
AACACCATAACCAGGGATGCCTTTGCACCCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGAATACCGGAAAAAGCCCCACAGGCCA
TCTCCCGCCAAAACCAATAAAGAGAGAGCCAGAGGGGACCACCGTGGATGGAGAACTTT
TGA

SEQ ID NO: 83_AI375137_H

ATGGGAAATTATAAATCTAGACCAACCCAACTTGTACTGATGAATGGAAGAAAAAGTC
AGTGAATCATATGTTATCACAATAGAAAGATTAGAAGATGACCTGCAGATCAAGGAAAAA
GAACTGACAGAACTAAGGAATATATTTGGCTCTGATGAAGCCTTCAGTAAAGTCAATTTA
AATTACCGCACTGAAAATGGGCTGTCTCTACTTCATTATGTTGCATTTGTGGAGGCAAG
AAATCACATATTCGAACTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAAT
GGATTTACAGCCTTGCAATTTAGCAGTTTACAAGGATAATGCAGAATTGATCACTTCTCTG
CTTCACAGTGGAGCTGATATACAGCAGGTTGGATACGGTGGCCTCACTGCCCTCCATATT
GCTACAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC
AATATTCAAGATGCAGTTTTTTTTCACTCCATTGCATATTGCAGCGTACTATGGACATGAA
CAGGTAACCTCGCCTTCTTTGAAATTTGGTGTGCTGATGTAAATGTAAGTGGTGAAGTTGGA
GATAGACCCCTCCACCTAGCATCTGCAAAAGGATTCTTGAATATTGCAAACTCTTGATG
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCACTCCAT
TTCTGTTCTCGATTGGACACCATGATATAGTTAAGTATCTGCTGCAAGTGATTGGAA
GTTCAACCTCATGTTGTTAATATCTATGGAGATAACCCCTTACACCTGGCATGCTACAAT

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FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG
GAAAACATCTTCAGTGAAACAGCTTTTCATAGTGCTTGACCTATGGCAAGAGCATTGAC
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG
CACACTGGATTACACTCTGCTTGCTACCACGGTCACATTGCTGCTGGTTCAGTTCTTACTG
GATAATGGAGCTGATATGAATCTAGTGGCTTGATCCCAGCAGGTCTAGTGGTGAAAAA
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTACACTC
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA
GGAGATGGCTCCTATGTGTCTGTTCCATCACCTTGGGGGAAGATTAAAAGCATGACAAAA
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCTTCACATTTCATCTTTCAGCTC
TCAGAAATTGAGTTCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG
TCAGATGTGGATATGTTTTGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCATCCCTGC
GTAATTCAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA
TACATATCAGGGGGTCTCTGTTCTCCCTCCTTCATGAGCAGAAGAGGATTCTTGATTTG
CAGTCTAAATTAATTATTGCAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG
ACACAGCCAATTATACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGG
CATGCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC
ATGACAAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACGCAGTGCCT
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT
GGCGAAATTCATTGCTCATCTCAAGCCAGCGGCTGCGGCAGCAGACATGGCTTACCAC
CACATCAGACCTCCCATTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA
GGGTGGAACGCATGTCTGAAGGAAGACCCGAATTTTCTGAAGTTGTCATGAAGTTAGAA
GAGTGTCTCTGCAACATTGAGCTGATGTCTCCTGCATCAAGTAACAGCAGTGGGTCTCTC
TCACCTTCTTCTTCTCTGATTGCCTGGTGAACCGGGGAGGACCTGGCCGGAGTCATGTG
GCAGCATTAAAGAAGTCGTTTCGAATTGGAATATGCTCTAAATGCAAGGTCCTATGCTGCT
TTGTCCCAAAGTGTGGACAATATTCCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG
CATTTTCATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCAGCTGA

SEQ ID NO: 84_H97685_H

ATGATTTCTTGCCCTGTNATAACCTATGCACTCACAAAGATGAACTCTCTGAGAGGGATGA
GCAAGAGCTTCAGGAAATCCGAAAGTATTTCTCCTTTCTGTATTCTTTTTCAAAGTGCC
GAAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAATGGAGAGCGAAAGATCACC
GCTTTATCGCCAGCTAATTGACCTGGGCTATCTGAGCAGCAGTCACTGGAACCTGTGGGGC
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGGAACAGAGTGAAAAGCTGAGACA
CTTGAGCACATTTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT
GAACCTGGTGCCTGCACTGCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAAGGAGAATGAGTTGTA
TGAATCATTGATGAATATTGCCAACCAGGAGGAAATGAAGGATATGATTGTTGA
GACACTTAATACCATGAAGGAGGAACTTCTGGATGATGCTACTAACATGGAGTTTAAAGA
CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG
ACAGATCCAGGAACTCATCATCTCCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG
CTCAGTGGATTACCTGAGGGAAAGCTTCGTCGGAACCCTGGAACGATGTCTGCAGAGCCT
GGAGAAGTCTCAGGATGTCTCAGTTCACATCACCAGTAATTATCTCAAACAGATCTTAA
TGCTGCCTATCATGTTGAAGTCACGTTTCACTCAGGGTCGTGAGTTACAAGGATGCTATG
GGAGCAAATCAAACAGATCATCCAGCGCATCACATGGGTGAGCCACCTGCCATCACTCT
GGAATGGAAGAGGAAGGTGGCCCAAGGAGCCATTGAGAGCCTCAGCGCCTCCAAATTGGC
TAAGAGCATTTCAGCCAATTCCGGACTCGGCTCAATAGTTCCACGAGGCTTTTGCAGC
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGGTTAGAGAAAACGGAAGATCTATG
GCTGAGGGTTCGGAAGATCATGCTCCCCGCTGGCCCGCCTTTCTCTGGAAGCCGTTG

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FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA
GTATGGTGTGGTATACTGTGTGACAACTGGGGAGGACACTTCCCTTGTGCCCTCAAATC
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTTCACTATATGAG
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTCAGTCATTGACTACAACATA
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA
CACAGGGCTGAAGGCTGGGCTGACCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT
GGAGGGAATCCGCTTCCTGCACAGCCAGGGACTTGTCCATCGTGATATCAAACCTGAAAAA
TGTGCTGCTGGATAAGCAGAACCCTGCCAAGATCACTGACTTAGGATTCTGCAAGCCAGA
GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCTGAACTTTTCAC
AGGGAAGTACGATAATTCCGTGGATGTCTACGCTTTTGAATTCTTTTCTGGTATATCTG
CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG
GAACAATGTGCGGAGGGGGGCTCGCCCAGAACGTCTTCTGTGTTTGATGAGGAGTGCTG
GCAGTTGATGGAAGCCTGTGTTGGGATGGCGACCCCTTGAAGAGGCCTCTCTGGGCATTGT
CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTTCACTCTCTAGTTATT
TCCTTCCCCCTCACCATTGCGCCATGGGGAGAATTTGACATTTATTCACTATAGGACACA
CTCCCAAGGGAACCTGGTGCTTGCTGGGAACTTGGAACTTCCCAGGCAGGGATGACTCC
TGGACAGTGAAGAGTTGAATGACTGAGCATATTGAGCAGCTCACTGAAGCGCCAAGCTAT
CCCTTTAGCAAAAAAGTGTCTCAGATGTGTAAAAGCTGAGGAATGTGGTGTCTGGCTTC
ACAAATGAAAAGGAGGCAGATGTT

SEQ ID NO: 85_W20810_M

TTGATGTCAACCTGAAGGCTTCTAAAGCGAGTGATGTCTACAGCTTTGGGATCCTCGTGT
GGGCAGTGCTGGCTGGCAGAGAAGCTGAGTTGGTAGACAAGACTTCACTAATCCGGGAAA
CAGTGTGTGACAGGCAGAGTCGTCTCCACTGACAGAGCTGCCTCCAGGTAGCCCTGAGA
CTCCCGGCTTGGAAAACTGAAGGAGTTAATGATTGCTGCTGGGGTTCCAGTCCGAAA
ACAGGCCATCCTTCCAGGACTGCGAACCAGCAATGAAGTTTACAATCTGGTAAAGG
ACAAGGTAGATGCTGCTGTCTCCGAGGTAAAGCATTATCTGTCTCAGCACAGAAGCAGCG
GCAGAACTTGTCTGCCAGAGAGCCAAGCCAAAGAGGCACAGAAATGGATTGCCCGAGGG
AAACCATGGTTTCTAAAAATGCTGGACCGCCTGCATTTGGAGGAACCCCTCCGGACCAGTTC
CTGGAAAATGTCCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAGCAA
GGACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCCTTCAGAG
GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCCTCACCCCAAAGGAATCAGG
GAGATGGAAGACACGGCACTCCTTGGTATCCCTGGACCCCAACGAATCCAATGACAGGGC
CACCGGCTCTCGTCTTCAACAACCTGTTCTGAAGTGACAGATTGGGAACTACAACCTCCTTG
TAGCACCACCAAGAACTACTGCCTCAAGTTCCGCCAAGTATGACCAAGCACAGTTCGGCA
GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAAGAAATCACTGCAAGAGCCTGA
AGTGTGCCATTGAGCGTGGCAATAAAAAGCACGTTTAAAGCAACCTGGACTGGCTAAGAC
AGTCCTTGCCACTTCTGAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAA
ACTGACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTAACTGTG

SEQ ID NO: 86_AA744236_H

ATGGGATCAGAGAACAGTGCTTTAAAGAGCTATACACTGAGAGAACCACCATTTACCTTA
CCCTCTGGACTTGCTGTTTATCCCGCTGTACTGCAAGATGGCAAATTTGCTTCAGTTTTT
GTGTATAAGAGAGAAAAATGAAGACAAGGTTAATAAAGCTGCCAAGCATTGGAAGACACTT
CGTCACCCTTGCTTGCTAAGATTTTTATCTTGTAAGTGTGGAAGCGGATGGCATTATCTT
GTCAGTGAAGGAGTACAGCCCTGGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCTTCTCATGACAGAGGACACCTA
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGACACTGGAAGCTA
GGAGGAATGGAACTGTTTGTAAAGTTTCTCAGGCCACACCAGAGTTTCTGAGGAGTATT

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FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCCAACT
CTCCCAGAGTGTGATGGACATGCCCGGGATGCCTTTTCATTGGAACATTGGTGAAAGT
TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC
TTGCACTCAACTTTGCTGAATCCCATTTCCAAAATGTGCGCCAGCGCTCTGCACCTTACTA
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAACA
TTGAAGAGTGAAGAGGAGAAAACGGAATTCCTTAAATTTCTGCTGGACAGAGTCAGCTGC
TTGTCAGAGGAATTGATAGCTTCAAGGTTGGTGCCTCTTCTGCTTAATCAGTTGGTGT
GCAGAGCCAGTGGCTGTTAAGAGTTTCTTCTTATCTGCTTGGCCCCAAAAAGATCAT
GCGCAGGGAGAAAACCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC
GTGCTTCTCCAGTTGTTTGAAGTTCATGAAGAGCATGTGCGGATGGTGTCTGTCTCAC
ATCGAGGCCTACGTGGAGCACTTCACTCAGGAGCAGCTGAAGAAAGTCATCTTGCCACAG
GTTTTGCTGGGCCTGCGTGATACTAGCGATTCCATTGTGGCAATTACTCTGCATAGCCTA
GCAGTGTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAACGAACCAAGATC
TTCAAACGCACTGCCCCAAGTTTACTAAAAATACTGACCTTTCTCTAGAAGGCGATCCA
TTTTCTCAGCCTATTAAATTTCCCATAAATGGACTCTCAGATGTAAAAATACTTCCGAG
GACAGTGAAAACCTCCCATCAAGTTCATAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA
CCTGAGGAGCCTGAAAATCAAACGTCAACATACAGATTTGGCCTAGAGAACCTTGATGAT
GATGTCAAGTCCCAGTGCCTACCTTGGATGTGGAAGAGTCATCTTGGGATGACTGCGAG
CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT
ACCTCAGGGGAGCAGAAGCCTATTCTGCTTTGCTTTCACTCACTGAAGAGTCTATGCCT
TGGAATCAAGCTTACCCCAAAAGATTAGCCTTGTACAAAGGGGGGATGACGCAGACCAA
ATCGAGCCGCCAAAAGTGTATCAACAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT
TTAGGAGAGGAATTCACCATTCAGTAAAAAAGAAGCCAGTAAAGATCCTGAGATGGAT
TGGTTTGCTGATATGATCCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA
CTGAGGACAGAAATGGTCCCCAAAAGGATGATGTCTCCCCAGTGATGCAGTTTTCTCA
AAATTTGCTGCAGCAGAAATTAAGGAGGAGGCTGAAGGCTGGGAAGAAGAAGGGGAG
CTGAACCTGGGAAGATAATAACTGGTGA

SEQ ID NO: 87_AI052250_H

AGCGGCCGCGGGGGCGGCGGAGGATATGGAGTAAAGCCAGAGTCAGTGGCCAGGCACGAA
GGCAGAGCAGGAACAGCCAGGAGGCGTTTATTAGGGGGGCGGGGGGAAAGAGCCCCAGCA
CCGCCCTCCTGGAAGAAGGAAGAGGTAACTATAACTACCAATATTGCAGCCATGGAGT
CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGCGG
TAATGGGAATTCCTGTCACTAGAGAATTTGATGTTGGTGCACACATTGCCAGTGGTTGCA
ATGGGCTAGCTTGGAAGATTTTAAATGGCACAAAAAGTCAACAAAGCAGGAAGTGGCAG
TTTTTGCTTTTGATAAAAACTGATTGACAAGTATCAAAAATTTGAAAAGGATCAAATCA
TTGATTCTCTAAAACGAGGAGTCCAACAGTTAACTCGGCTTCGACACCCTCGACTTCTTA
CTGTCCAGCATCCTTTAGAGAATCCAGGGATTGCTTGGCATTTTGTACAGAACCAGTTT
TTGCCAGTTTAGCCAATGTTCTTGGTAACCTGGGAAAATCTACCTTCCCCTATATCTCCAG
ACATTAAGGATTATAAACTTTATGATGTAGAAACCAAATATGGTTTGCTTCAGGTTTCTG
AAGGATTGTCACTTCTTGATAGCAGTGTGAAAATGGTGCATGGAAATATCACTCCTGAAA
ATATAATTTTGAATAAAAGTGGAGCCTGGAAAATAATGGGTTTTGATTTTTGTGTATCAT
CAACCAATCCTTCTGAACAAGAGCCTAAATTTCTTGTAAAGAATGGGACCCAAATTTAC
CTTCATTGTGTCTTCCAAATCCTGAATATTTGGCTCCTGAATACATACTTTCTGTGAGCT
GTGAAACAGCCAGTGATATGATTCTTTAGGAACTGTTATGTATGCTGTATTTAATAAAG
GGAAACCTATATTTGAAGTCAACAAGCAAGATATTTACAAGAGTTTCAGTAGGCAGTTGG
ATCAGTTGAGTCGTTTAGGATCTAGTTCACTTACAAATATACCTGAGGAAGTTTCGTGAAC
ATGTAAAGCTACTGTTAAATGTAACCTCCGACTGTAAGACCAGATGCAGATCAAATGACAA
AGATTCCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC
AAAGAGATAATCTTCAGAAATCACAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAAC

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FIGURE 2RRR

TGCCCAAGCGTGTCATTGTGTCAGAGAATTTTGCCTTGTGTTGACTTCAGAATTTGTAAACC
CTGACATGGTACCTTTTGTGTTTGGCCCAATGTTCTACTTATTGCTGAGGAATGCACCAAAG
AAGAATATGTCAAATTAATTCTTCCTGAACCTGGCCCTGTGTTTAAGCAGCAGGAGCCAA
TCCAGATTTTGTGTTAATTTTCTACAAAAAATGGATTTGCTACTAACC AAAACCCCTCCTG
ATGAGATAAAGAACAGTGTTCTACCCATGGTTTACAGAGCACTAGAAGCTCCTTCCATTC
AGATCCAGGAGCTCTGTCTAAACATCATTCCAACCTTTGCAAATCTTATAGACTACCCAT
CCATGAAAAACGCTTTGATACCAAGAATTAAAAATGCTTGCTACAAACATCTTCCCTTG
GGTTCGTGTAAATTCATTAAACAACATTGGAGCAGACCTTCTGACTGGCAGTGAGTCCG

SEQ ID NO: 88_AA278842_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCCCCGGCTCGGGCGGCCGGAG
GACCCGGAGCTAAGGCGCCGAACCCGCGGGCGGGTGGGGACGATGTGGTTCTTTGCC
GGGACCCGGTCCGGGACTTTCCGTTTCGAGCTCATCCCGGAGCCCCAGAGGGCGGCCTGC
CCGGGCCCTGGGCCCTGCACCGCGGCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA
AGCGCTTCAAACTCTACGGCACCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG
AAAAATGCCTCCACGTCGTGACAGAGGCTGTGACCCCGTTGGGAATATACCTCAAGGCGA
GAGTGGAGGCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGTGA
AAGCCCTCAGCTTCTGGTCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCG
CCGTGTTCTGTGGACCGAGCTGGCGAGTGGAAGCTTGGGGGCTGGACTACATGTATTCCG
CCCAGGGCAACGGTGGGGGACCTCCCGCAAGGGGATCCCCGAGCTTGAGCAGTATGACC
CCCCGGAGTTGGCTGACAGCAGTGGCAGAGTGGTCAGAGAGAAGTGGTCAGCAGACATGT
GGCGCTTGGGCTGCCTCATTGGAAGTCTTCAATGGGCCCCTACCTCGGGCAGCAGCCC
TACGCAACCCTGGGAAGATCCCCAAAACGCTGGTGCCCCATTACTGTGAGCTGGTGGGAG
CAAACCCCAAGGTGCGTCCCAACCCAGCCCGCTTCTGCAGAACTGCCGGGCACCTGGTG
GCTTCATGAGCAACCGCTTTGTAGAAACCAACCTCTTCTGGAGGAGATTAGATCAAAG
AGCCAGCCGAGAAGCAAAAATTCTTCCAGGAGCTGAGCAAGAGCCTGGACGCATTCCCTG
AGGATTTCTGTGCGCACAAAGGTGCTGCCCCAGCTGCTGACCGCCTTCGAGTTCGGCAATG
CTGGGGCCGTTGTCTCACGCCCCTCTTCAAGGTGGGCAAGTTCTGAGCGCTGAGGAGT
ATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGC
GCATCCGCCTCCTGCAGCAGATGGAGCAGTTCATCCAGTACCTTGACGAGCCAACAGTCA
ACACCCAGATCTTCCCCACGTGCTACATGGCTTCTGGACACCAACCTGCCATCCGGG
AGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATG
TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA
GGGTCTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGACCCGTCCCGGGTTG
CGGGTGTCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGA
AGATCCTGCCTGTGCTCTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGG
CCTTCAAGGCCATTCCGAGCTTCTGTCCAAATTGGAGTCTGTGTGCGAGGACCCGACCC
AGCTGGAGGAAGTGGAGAAGGATGTCCATGCAGCCTCCAGCCCTGGCATGGGAGGAGCCG
CAGCTAGCTGGGCAGGCTGGGCCGTGACCGGGGTCTCCTCACTCACCTCCAAGCTGATCC
GTTTCGACCCCAACCACTGCCCCAACAGAAACCAACATTCCCCAAAGACCCACGCCTGAAG
GAGTTCTTGCCTGCCCCAGCCCCACCCCTGTTCTGCCACCCCTACAACCTCAGGCCACTGGG
AGACGCAGGAGGAGGACAAGGACACAGCAGAGGACAGCAGCACTGCTGACAGATGGGACG
ACGAAGACTGGGGCAGCCTGGAGCAGGAGGCCGAGTCTGTGCTGGCCCAGCAGGACGACT
GGAGCACCGGGGGCCAAGTGAGCCGTGCTAGTCAGGTGAGCAACTCCGACCACAAATCCT
CCAAATCCCCAGAGTCCGACTGGAGCAGCTGGGAAGCTGAGGGCTCCTGGGAACAGGGTT
GGCAGGAGCCAAGCTCCAGGAGCCACCTCCTGACGGTACACGGCTGGCCAGCGAGTATA
ACTGGGGTGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCCTGTCTGCACGTC
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

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FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCCGGAAGAAGCGCGAGGAGCGGCGGCGGGAGA
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCGGA
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGCTGCGGAGAGCCCGCCCCACAGATGT
ATTTATTGTACAAACCATGTGAGCCCGGCCGCCAGCCAGGCCATCTCACGTGTACATA
ATCAGAGCCACAATAAATTCTATTTTAC

SEQ ID NO: 89_AA599286_H

ATGGCCTTCATGGAGAAGCCGCCAGCCGGCAAGGTGCTGCTGGACGACACGGTGCCGCTG
ACAGCAGCCATCGAGGCGAGCCAGAGCCTGCAGTCCCACACGGAATATATTATTCGAGTG
CAAGGAGGAATTTCTGTGGAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCTCCCAAAAAATTG
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTAGAT
CCAAACAACTATTCCGCAAACTATACTGAGATTGCCTTGCAACAGGTTTCCATGTTCTTC
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACTTTGAAAGACATAGGTTGGAGAATAAGG
AAGAAATATTTCTTGATGAAGATTAAAAATCAGCCAAAGGAACGGCTAGTGTTAAGCTGG
GCTGACCTTGGCCCAGACAAGTATTTGTGAGATAAAGATTTTCAGTGTCTAATCAAACCTT
CTGCCTTCTTGTGTCACCCTTACATCTATCGGGTTACCTTTGCCACAGCTAATGAATCC
TCAGCGTTGCTAATTAGGATGTTTAAACGAAAAGGGAACATTGAAGGATCTGATCTACAAG
GCAAAACCAAAAGACCCATTTCTAAAGAAGTACTGCAACCCTAAGAAGATTTCAGGGCCTG
GAACTCCAGCAAATAAAAACATATGGACGGCAAATATTAGAGGTACTGAAGTTTCTTCAT
GACAAGGGATTCCCTTATGGGCATCTTCACGCCTCCAATGTGATGCTCGATGGGGACACT
TGCCGGCTGCTGGACCTTGAGAATTCCTTATTGGGCCTGCCTTCTTCTACCGATCTTAT
TTTTCACAATTCAGGAAAATCAATACATTGGAAAGTGTGGATGTCCACTGCTTTGGCCAC
TTACTGTATGAAATGACTTATGGACGACCGCCAGACTCGGTGCCTGTGGACTCCTTCCCT
CCTGCCCCGCTCCATGGCTGTGGTGGCCGCTGTTGGAGTCTACGCTGTCTTGTGAAGCCTGT
AAAAATGGCATGCCTACCATCTCCCGGCTCTTACAGATGCCATTATTCAGCGATGTTTTA
CTAACCACTTCTGAAAAACCACAGTTTAAAGTCCCTACAAAGTTAAAAAGAGGCATTGAGA
ATTGCCAAAGAATGTATAGAGAAGAGACTAATTGAGGAACAGAAACAGATTCCACAGCAT
CGAAGACTGACAAGAGCTCAGTCCCACCATGGATCTGAGGAGGAAAGAAAAAAGAAAG
ATTTTAGCTCGAAAGAAGTCAAAACGATCTGCTCTTGAAAATAGTGAAGAGCATTACGCG
AAGTACAGCAACTCCAATAATTCAGCAGGATCTGGGGCCAGCTCACCTCTCACGTCCCCG
TCATCGCCAACTCCACCCTCTACATCAGGGATATCTGCATTACCTCCACCTCCTCCACCT
CCACCACCACCAGCAGCTCCCTTGCCCTCTGCGAGCACCGAGGCACCTGCCCAGCTCTCG
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCCCTTGCTCAGCTCCATCCAGAATTTCAA
AAAGGAACTTTGAGGAAAGCCAAACCTGTGATCACAGTGCTCCGAAGATCGGCTGAAGCT
TCCTGTTTACACTTGGAGGGAAAAGTTCTTTTTTATTCTACTACCCCTACCCCCAAC
TACCCTCTTCTGGGAAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC
AGATGCTCATGTAAGCAGCTTTTCGAGAGAAATAATTCTTTAAGCAGAATAAAGTTAGGC
TGGCATGCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 90_AA425725_H

ATGAGCGCCAGCACGGGCGGTGGTGGGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC
TCACAGGCCTCCTGCGGGCCCGAGTCTCGGGCTCCGAACTAGCCCTGGCCACACCGGTG
CCTCAGATGCTGCAGGGCCTTCTGGGCTCCGACGACGAGGAACAGGAAGACCCCAAGAC
TACTGCAAGGGCGGCTACCACCCTGTGAAGATCGGCGACGTGTTCAATGGGCGGTACCAC
GTGGTGCACAACTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCGGGGCATTACACGGAGACAGCT
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCAGTGACCCCAAAAGA
GAGACCATTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

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FIGURE 2TTT

TGCATGGTGCTGGAGGTGCTGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACTAC
CAGGGCCTGCCCGTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCGAGAACATCTTGCTG
TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGCCACGGAGTGGCAACAGGCA
GGGGCGCCGCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCAGGAGGTCTTGACCGGT
AAGCTGTCCAAAACAAGAGGAAGAAGATGAGGCGCAAACGGAAACAGCAGAAGCGGCTG
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT
GAGGACTCTGGCTTGAGACTAGACGGGGGCGAGCGGCTCCACATCCTCTTCAGGCTTCTCC
GGCTCCCTCTTCTCTCCTGCCTCCTGCTCCATCCTCTCCGGCTCGTCCAATCAGCGAGAG
ACCGGGGGCCTCCTGTGCGCTAGCACACCATTCCGTGCCTCGAACCTCCTGGTGAACCCC
CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC
GAGCTGGCCACTGGTGACTACCTGTTTCGAGCCGCATTCTGGAGAAGACTACAGTCGTGAT
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGGACATCCCCCAGCCTTCGCCCTC
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT
CTCAAGCACTGGGGCCTGTACGAGGTACTCATGGAAAAGTACGAGTGGCCCCCTAGAGCAG
GCCACACAGTTCAGCGCCTTTCTGCTGCCCATGATGGAGTACATCCCCGAAAAGCGGGCC
AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

SEQ ID NO: 91_SGK022_H

TCTGGCCCTGTCCCTCCCCACCACCCGCGCTGTGTCCAGACAGAGAATGTTCTAACGCT
GGGGGCGGCTGCGGATGAAGTCCTTGGGGAGAAAAGGAGCAGGCCAAGGGCGATGGTGGA
GTAGAGCTGCCTCTCAGAGGCAGCATGAGCTGAGAGGGTGATAGGAAGGCGGCGCTAGAC
AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAAGGG
ACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAACACCAAAGAAAAGTGGCAATTAAA
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCCCTCCCTCGGGAGCTC
CAAATCGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT
GCGGACGGGAAAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC
GTGCTGAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTGAGATGGTT
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGGCCACCGGGACCTCAAATGTGAGAAC
GCCTTGTGTCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCC
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAG
GTGCTGCAGGGCATTCCCCACGATAGCAAAAAGGTGATGTCTGGAGCATGGGTGTGGTC
CTGTATGTCATGCTCTGTGCCAGCCTACCTTTTGACGACACAGACATCCCCAAGATGCTG
TGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT
AGTTGGCATCCATGGCTAGCAAGCACTTGATAAAAGCAATGGCAAGTGCTCTCCAATAAA
GTAGGGGGAGAAAAGCAA

SEQ ID NO: 92_AA060026_M SGK022_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGGGGGGAAAAGA
AGCAGGCCGAGGGCGATGGTGGAGTAGAGCTGCCTCGCAGAGGCAGCATGAGCTGAGAGG
GTGACAAGAAGGAGGCGCTACACAGCATGGAGGACTTTTCTACTCTCCAATGGGTATCAGC
TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAAC
ATCAAAGAAAAGTGGCAATTAAATATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC
AGAGATTCTGCCTCGTGAGCTCCAGATTGTCCGTACCCTGGACCACAAAAACATCATCC
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAAATCTACCTGGTGATGGAACCTGCCTG
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGCCA
AGGCCCTCTTCCGCCAGATGGTTGAGGCTATTGCGCTATTGCCATGGCTGTGGCGTGGCCC

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FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA
GCACAGCCTATGCCGCCCCCTGAGGTGCTACAGGGCATAACCCATGATAGCAAGAAAGGTG
ATGTCTGGAGCATGGGTGTGGTCTGTATGTAATGCTCTGTGCAAGTCTACCTTTTGATG
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC
TCCGGCCTTCAATCGAAGAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC
AATGGCAAGTCTCCCCAATAAAGTAGGGGGAGAAAGCAAAGTCTG

SEQ ID NO: 93_AA399669_H

CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGCACTTCATTCTCAA
GTTTTGTGGCCAACGATGGATAGGAGGTGGATTGTGATGTATTTCGGAACATGGGACCTTG
AGGAGTTCCGTAACCAAAAGGAGAAAGTAACAACAGCCAGTGGAGACAAAAAGAACTGCT
TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGGAGGGCTGAGTCCAGCATCCCAGACTCGT
GTGACTATATAGGCAAGCATTGTTGGGGACCTACTTCACTTTGATACCTAGCCTTCAGCAG
CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA
AGCCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACCACAGCCTACC
ATTCCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCCGTGAAATACAGGTAA
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC
GAGTATACATCATCTGGAAGTGGCTCAGGGTGGTGTATGTCCTTGAATGGATCCAGCGCT
ACGGGGCCTGCTCTGAGCCCCCTTGCTGGCAAGTGGTTCTCCCAGCTGACCCTGGGCATTG
CCTACCTGCACAGCAAGAGCATCGTGCACCGGGACTTAAAGTTGGAGAACCCTGTTGCTGG
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTGGCTTTTCCCACCTCAGCCAGA
CTTACTGTGGCAGCTTTGCTTACGCTTGCCCAGAGATCTTACGAGGCTTGCCCTACAACC
CTTTCCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTACACTCTAGTGGTTCGCCCATC
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT
TCCCAGCTAACCATACCATCTCCCAGGAGTGCAAGGTCCAAGTGGCTCATTGCCTGTGTGG
CACAAATGGAGAAAACTCAGGCAAGACCTCTCTCTCCCCTGCTCTAGAACCCTGATCCTCC
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATCTTGGACATCATCAAGGATTCTTGGG
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC
AGCTCCAACAACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94_AA758539_H

GACCATTGACAGCCTCCGGTAGTGTAATGAGGACAATGCCTGCTGGCCCACATGACGG
GGGGATGTAGACGGCAGCGGCCAGTCGCTCCTGGCACCATGGACGATGCCACAGTCCT
AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGCAAGGGTTCTACGCAAAAGTCAA
ATCTGCCTACTCTGAGCGCCTCAAGTTCATGTGGCTGTCAAGATCATCGACCGCAGGAA
AACACCTACTGACTTTGTGGAGAGATTCTTCTCCTCGGGAGATGGACATCCTGGCAACTGT
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC
CCTGCATGAGGACGTGGCAGCAAGATGTTCCGACAGCTCTCCTCCGCGTCAAGTACTG
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGAGAACCCTTCTCCTCGACAAGGA
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTCGGCAGCATATGCAGCCCCGAGGTGCT
GCAGAGCATCCCCTACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

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FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA
CCTCATCTACCGCATGCTGCAGCCCCGACGTGAGCCAGCGGCTCCACATCGATGAGATCCT
CAGCCACTCGTGGCTGCAGCCCCCAAGCCCAAAGCCACGTCTTCTGCCTCCTTCAAGAG
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAACCTGGACACCAAGACAGGCTTGAGGCC
CGACCACCGGCCCGACCACAAGCTTGGAGCCAAAACCCAGCACCGGCTGCTGGTGGTGCC
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG
TGGTGGGGGTTCGGGGTTGGGGGGCATGGTGCAGTCGGCCTTCACGTAAACTAAGTAGGCA
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAAATTTCGTCAATTAAACCACTATTTTGA
TT

SEQ ID NO: 95_AA883975_H

ATGTCTGGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCCGCACAATTGGAGAG
GGCAGCTACTCCAAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATC
AAGGTGGTGGACCGGCGGCGAGCGCCCCCGACTTCGTCAACAAGTTCCTGCCGCGAGAG
CTGTCCATCCTGCGGGGCGTGCGACACCCGCACATCGTGACGTCTTCGAGTTCATCGAG
GTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC
GTGCAGCGCAACGGGCGCATCCCCGGAGTTCAGGCGCGCGACCTCTTTCGCGCAGATCGCC
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCAGAAAC
GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG
GCCCCATGGCTACCCAGACCTGAGCACCACTACTGCGGCTCAGCCGCTACGCGTCAACC
GAGGTGCTCCTGGGCATCCCCTACGACCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC
GTGCTCTACGTATGGTCAACGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
AAGGCCCTGATCGCCGAGCTGCTGCAGTTCAGCCCGTCCGCCAGGCCCTCCGCGGGCCAG
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGACTCCGGCTAG

SEQ ID NO: 96_AA905446_H

CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA
TCATGGAAAGAATTGTGGGGTCAGGGGACAGTGGCGGGAGGAGCTGGCTCACCACCTGT
GGACAAATCAGGCCTTATAATTTGTGATTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC
TTTTGAATGATATACTAACGACAAAAATAATAGAAGTGAACATTCTTTGCAATGTCCAAG
CAGCTAGACACACTTAAGACCATTAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC
AGAAATTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCTTTCTGATCTGCCAGCCCAT
CTCTCCTCCCCTTACTTCCTCAGAGTTTATCCAGAGATTCTCCTCCCTCGGGAGCTCCAAAT
CGTCCGTACCCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCTGCCGA
CGGGAAAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT
GAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTCAGATGGTTGAGGC
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT
GTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCCAAGTC
ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT
GCAGGGCATTCNNCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGCTTCCCCACTCA
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC

FIGURE 2WWW

SEQ ID NO: 97_H29974_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCAGTGGC
CGGGCGCAGCGGGGCCGGGTGGCGGTCAAGAAGATCCGCTGCGACGCCCCGAGAACGT
GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT
CGTGCACTTTGAGGAGTGCCTCCTGCAGCGCAATGGGTTAGCCCAGCGCATGAGTCACGG
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGTTTGTTCATGGAGTTCTGTGAAGGTGG
AGACCTGAATCAGTATGTCCTGTCCCGAGGCCAGCCAGCCACCAACAAAAGTTTCAT
GCTACAGCTGACGAGCGCCATTGCCTTCTGTCACAAAAACCATATTGTGCACAGGGACCT
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGA
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTTCGGACTTCTA
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCT
AGAAAAACCCAAAGATGGAGTTGCACATCCCCAAAAACGCAGGACTTCCATGTCTGAGGG
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCCTGATGCCTT
TGAACCTGAAACCAGAATGGACCAGGTACATGTGCTGCTTAAAATTACAGGGCTAAGCAT
TTTGGGTGATTTTAAACTAGGTGATTCTCGGGACCCACAGTCTCACCAGTCTCCTCC
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGTTGGCGATCTCCCGACAGCTGGA
TCCGGCAATGTGAAGCTTTTGTGTTGGGTTTCCCGCTTCTTTTAGTTTGTCTTTATTN
TNNCCTTTTCTTTTCTTTTTTTNTTNNCCACNTNCCTTTTTTTAAATTTAAACCATTGAG
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTTATAAGGGGTTAGGGAGCTAT
TTTTGGTTTTGTCTTCACTTTCCCTCTGTCTTCTTCTTTATACTTTCTCAGTTCTAC
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCCATAGGGAATCTGGGGGTANCT
TCTGGAACGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG
GAACTCCTGGACTCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA
GAGGTGAAGAACCGCC

SEQ ID NO: 98_AA498104_M H29974_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCGC
AGAGGGACAAAAAGCCCGGAGCGGAAAAGGCGAAGCCAGTCCAGCGGGTACTGTGCGAG
AAGCTGAGGCCGGCGGCCAGGCCATGGATCCGGCTGGGGCCGAGGTCCCGGGCGAGGCC
TTCTGCCCCGGCGGCCGGATGGCGGCGGCGGGATGTTCTGCACGGCCGCGCTAC
AGCCTCTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCTGTGGCTGGG
CGCAGTGGGGCCAGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCCGAGAACGTGGAG
TTGGCACTAGCAGAATTCCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG
CAGTTTGAGGAGTGCCTCCTACAGCGCAACGGGTAGCCCAGCGCATGAGTCACGGCAAC
AAGAACTCACAGCTTTACCTGCGCCTGGTGGAGACCTCGCTCAAAGGAGAAAGGATCCTG
GGCTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTACTGTGAAGGTGGAGAC
CTCAATCAGTATGTCTGTCCCGGAGACCTGACCCAGCCACCAACAAAAGTTTCATGCTA
CAGCTTACAAGCGCCATTGCCTTCTGTCATAAAAAACCATCGTGACAGGGACCTAAAG
CCAGACAACATCCTGATCACAGAGCGGTCTGGCACCCCCATCCTCAAGGTGGCAGACTTT
GGACTGAGCAAGGTCTGTGCAGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGATAAC
AAAAATGTGAATGTGAATAAATACTGGCTGTCTCAGCTTGTGGCTCAGACTTCTACATG
GCTCCCGAAGTCTGGGAGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC
CTGGGGACCTACATTAAGCAAGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCTAGAA
AACCCAAAGATGGAGTTGCATATCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGGTC

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FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA
CTTGAAACCCGAATGGACCAGGTACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG
GGTGTTTTTTAACTAGGTGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA
TGGCAGAGGGTACAGGTGGTGGTGATCTCCTGACAGCTGGACCTCCCAATGTGAAGCT
CACGCTTGGGCTGCCACTCTACCCTTCTCTTTCTCCTTCAGTAGAATAATAATTGTTTT
TCTAAACATTAAACCATCAAGACTTCTGAAGAGCAGAAGGCTACACTCTG

SEQ ID NO: 99_AA215311_H

CGRCCGCGCTACGGAAGCCGGAGGGGGCGGGGCCGTGCGCGTAAGGGGGTGTGTCCGC
GCGCACACCGGGGCGCGCGCCGGCTGCTGACTGGAGGCGGCGGCAGCGGAGGCGCGAGC
TGCCCCGATAATGGCGGCCTGCAGAGCCCATGAGAGGGAGAAGCGGCAGCGTCTACCCTGA
GAAACCTCGACCTTGAAGATGGTGAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG
GCAGTGAAGAAAATTCGATGTACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC
TGGGCACTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC
CTACAAAAGGATGGGATGGTGCAAAAGATGTCCACGGCTCTAATTCTTCCCTTTATTTA
CAGCTTGTAGAACTTCATTAAGAGGAGAAATTCCTTTGATCCCAGAAAGCGCCTATTAT
TTGTGGTTTGTGATGGATTTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG
AAGCCCAATCGTAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC
TTGCATAAAAACCAGATCATCCACCGAGATCTTAAGCCTGATAACATCCTGATTTCTCAA
ACCAGGTTGGATACCAGTGACTTGGAACTTACCCTCAAAGTGGCTGATTTTGGTCTAAGT
AAAGTTTGTTCAGCCTCTGGGCAGAACCCAGAAGAACCTGTGAGTGTAACAAGTGTTC
CTTTCACAGCATGTGGAACAGATTTTACATGGCTCCTGAAGTTGGGAAGGACATTAC
ACAGCAAAAGCTGACATCTTTGCTCTGGGGATTATCATCTGGGCAATGCTGGAAAGGATC
ACATTCATAGACACAGAGACAAAGAAGGAACTCTTGGGGAGTTATGTAAACAAGGAACT
GAGATTGTGCCTGTTGGGGAGGCACTTCTGGAATCCCAAAATGGAACCTCTCATTCCCT
GTGAAGAAAAAATCTATGAATGGGCGAATGAAACAACCTGATTAAGGAAATGCTGGCTGCA
AACCTCAGGATCGTCCAGATGCTTTTGAAGTAGAACTCAGATTAGTACAAATTGCATTT
AAAGATAGCAGCTGGGAAACGTGACACATATTATTTGCAATACCATGGATGATATGCTG
CTTCTGTTTAAACAGTGATGCAACATTATGTGGCTGAAAAAGAATATAAAAAGCTAGACTC
TACCTCTAAGGGTTTAGATTTTTTGTGGGATTTTTTTTTCTCATTCTTTCTTAAATCC
AAGTTGGCCGTTTTATTAGTATGTTTCAAATGTGTATTACCAATGTGGGTGTAAATTTTT
AAAAATGATTATTGATAGAAGTTTGGCAGGAAATCTTTAAGAGCTAACAGAGAAGA
GAGTCCAGTTTTCTGGAATATGTCTTTAAGTATTTTAGACATTCCTCGTCAGTATTAGG
AATTTCCATGGGAAAGAGGTTTGCATGCTGGTAATGCAACCTTTGAACTTTGTAAAGG
AAACATATATGTATATATTTATGTATATGTAAGTATGTGAATGTGCGCATTTTGCATTCC
ATATGAAAAAATGCCACGTCTGTTTAAATTATTTGATGTAGGTTGGGTTTTTGAGATT
TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCTACTCTGCCCCCTCC
CCTAATGAAATCATATTAAGTNGTTTTCTCTNNTTTTTTTGTAATATACAGCTTTTTTTT
TAAGGCATCATTTTCGAGGGTCTAAAATTATCTGGTAAACAAATGAAATTAAGTGATCC
AAAGCTGCTGAAGTATGTTTGAAGTCTCCAGTGCCCTATAGCTGCAAGAGTTGAATTAGT
CATGCAGTCATATGGCAGCAGGTTGGTGATT

SEQ ID NO: 100_AA018361_H

GCGGGGCTCCGTATCCCCACGTGGGCCCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG
AGGCCAGAGACAGGGGAGGGGCGCCGGGAGCCGGGCGGATCCGCGTCCCCGATGCGCGC
TGCAATTCGCGCGGGCGCGCTGGGGGCGAGCGTGAGCCACCCAGTGCTCGGCCCCGCCCC
GCAACCCGCGGAACCGCCCGCCCGCAGCGAGGAAGCGCCCGCGCGGCGAGGCGGCCG
AATGGCGGGGCGCGCTGGGGTCCCCCGCGCTGGACGGCTTCATCCTCACCAGCGCCT
GGGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

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FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAAGAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT
CACGGAGATTGAGATCCTCAAGGGCATTTCGACATCCCCACATTGTGCAGCTGAAAGACTT
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTCGCGAGGGGGCGACCTGTC
TCGCTTCATCCATACCCGCAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA
ATTAGCTAGCGCCCTGCAATTCCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC
ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAAACTGGCAGACTTTGGTTT
CGCACAACACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT
GGCCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCCGCTGGACCTCTGGTCCATGGG
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTCGTTCTCGGA
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCCTTGCAGCCCCCTGCTCTC
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTCGCATCTC
CTTCCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAG
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATTTC
AGCAGCCGCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGCACTA
TGAAGTGGATGCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCCG
GGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGAGGCAGGGGAC
CTCTGCCCCGAGACCTGCTCAGAGAGATGGCCCGGACAAGCCACGCCTCCTAGCTGCCCT
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGGCCCGCGGGGAGCAGGATGCCCT
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCCGGGCCGG
AGGCGGGAGCTGCTTCACACTGAGGTTTCAAGCCTCATGGCCCGAGCTGAATACTTGAAG
GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAGAGGGACTGTCCGAA
TCTGTTCTGTAGCTCTTGACCCCTTCACTGACCCTAGAAGAATGATTGGACAGATGTGAGC
CATCTGGAGCAGAGGGGCACCTAACCCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG
CCCTGGCGAGCAGGCTTCTTGGATGGACAGTGTGAGACCCCATATCCCAGAGTCCCCA
GCCTCCCTCAGGTTACTCTGCACCCACAGATGGTTTGATGGCTGTGCTGTATACTGGAG
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTTCATGAGACCTTTGTTACTCGGTGGT
TACTGGGTCTGTGCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTTGGCTCCGA
GAAGAGGGCAAGGGGCCCCCGCAGGGTACTTCTGTGCTTGGCCCTCGCCCTGCCAGCAGGC
AGCTGTGCCCCCTGGCTGCCCTTCCCGGGACCCCTTATTCCAACCTCAGCTCCTCTTTGCA
CTGGAATGGGGCACTCCAACACCCCTCAGGGACCAACCTCCCCACAGTATGCACTCAGCC
CCACAGAACCCACCAGTCTTTCTGGGAACCTCACACCTGCCCGCCATCTTGGTACTTTAGG
TTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTTAAGAAGCCCAAGCCTTGTTCC
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCCTTGGTCTCTATCTCTCCACCTCCGTT
CCCTCTGGGCCCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGGAGCTGGGACA
GGGAGAGGGAGGCTTGGAGACAGTCTGACCCAGTGGCCCTCTAGGCCACCCACTTCTAGGC
CTGCCCTGCCGCGGTGGAGCCCTGGGCAAGCTCTTCCCCCTTCTGGGCCTGGGTCTCCC
CATCTCTTCAATGGGGCTGATACCTTACAGCCACAGCATGGGCACTTATGAGGACAAA
GTGAATTTAACCCTGGAAAAGAATGTATTTGAGAGTTTCTTTTAAATAATCAGCGGGTGT
GGTGATTTGTAGCCCTTCTGCCCTTAAATGCTTCTTGGGCAAGAGCTGTCTGTCTCTCC
TGCAGGAGGCTGAGTGTGAAGAGTATCATTCAATTGTTTCTCTATTAAATTATTTCTCT

SEQ ID NO: 101_AA311714_H

TGGACCTGTCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT
GGACTCTTTTCTTGACTTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATCGTATGTGA
GAAGTCGGCCAGAGATGGAAAACCTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTTGTAGCCATTCTTTGTACT
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTACCCCGTGAAATAAAACAC
AAGAATATTGTAACCTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT
GAAAACCTCCCGAAGATGTTGTGAGAGAATTGGAATTGACCTGATTAGTGGATTACAT
CATCTTCATAAACTTGGCATTCTCTTTGTGACATTCTCCTAGGAAGATACTCTTGGAA

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FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGATAATGGGGAAAATGTC
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT
GAAATGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTGTTCAGAATTAAC TGAAAAG
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAAGATTCTTCTCGTCTAAAGCTTCT
TCAGATTTTATTAATTTGCTTGATGGGTACTTCAAAGAGATCCTCAGAAAAGATTGACT
TGGACAAGGCTACTGCAGCATTCATTTTGGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA
TCAAGCGTCGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTCTGGGCCACAAGAT
TCCAAGGAGCTTTTGCCAGAACTCTCAGAGTAGACAAGCAAAGGGCACAAGAGTGGTCAA
CCACTAGGTCACTCTTTCAGACTAGAAAATCCAACTGAGTTTCGGCCTAAGAGTACTCTT
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCTACTCCAGAAGTACTAGC
ACTGCAGTGGAAAGTAAGTCCCTGGTGAGGATATGACTCACTGTTTACCACAGAAGACTTCT
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCAGATGAGA
GAGCTTATCTACACGGACTCAGATCTTGTGTGTCACCCCCATTATCGACAATCCAAAGATA
ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTTCAGTG
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTTGCAACAAGTGTGCTCG
CAGATCGACTCCACTGAGAAGAGCATGGGGGCTCCCGAGCCAAGCTGAATCTCCTTTGTC
TATTTGTGCGTGGTGGCTGGTCCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTG
TTCCAATTGCTAATCCAGCATTGCGGATAGTCTCCAACTGGGATATACGGGCCAAGGTT
GCTCAGCTGATTGGTTTACTGGCTTCGCACACAACCTGAGCTCCAGGAAAATACACCTGTT
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCACACTCCACT
CCAGTGCCTAGACAGTGCCTTGTGTATGTATAGATACTGACAAATATTTCAAATAAATA
AAACTGTATCAGCATT

SEQ ID NO: 102_SGK384_H

TCTTTGGCCCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC
CTGCGGGGCTGGTTCAGCGGCCTGCGCTACCTGCACCAGCGGTGCATCCTGCACCGC

SEQ ID NO: 103_AA210451_M SGK384_M

GGTCTGCTGCATGGATAATGGACTGGAACACAGAAAGACCATGCAGGGTTCGGCTGTAGA
AGGCCAGTATCTCCAGAGGCCAGAAGACACCATCAGATCTCCTGGGACTGGAGTTATAGA
GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA
AACCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCGGGGCTGGGGCTGCTGCTCGCCATGG
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCCTGGACGAT
CCACCGCGGACTCTAGGCGCTGTCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT
GCTCAGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT
CCCGGCTCACCAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTTC
TCACCGAATATCACCCCTTAGGTTCTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTGAGCA
TCATTAACATATCTGCATCACAGCCCCCTGGGCACGAGGGTCATGTGTGACTCTAACGACC
TGCCCAAACATTGTCCCAGTACCTGCTAACAAGTAACTTCAGCATTGTGGCAAACGACC
TGGACGCTCTGCCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT
TCCAAGACGATCTCATGCCCTTCTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG
TCTCCAGTTTCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTTG
ATATCCATAAGGCGTGCAAGAGCCAGATCCCCGCAGAAAGACCCACTGCTCAGAACGTGC

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FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTCGCAGACGAAAG
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTTCAGCC
ACGTAGGCCTCCTCTACGTCTGCCTGCATGTTTGAGTGTTCTGCTCTCCTGGCAGCCCGG
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG
ATTCTGGATCTGCATAGTTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC
TGCCTTGGTAACTTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGAC
AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTAGAAAGCCCTGTTGGAAGCTGGG
GATGTTTTAACTCCGTGGCAGGGCACTTGCCTAGTTGTGTGCAAAGCCTTGGATCTGACC
CATGGCATGTGCACACACACAAATGCTCAAAGAAAATCCCAGACGCCAGAAGTGTGCCCC
TTTCTTGTCAATAAGGTCATTGTGCTAGTACCGGAGATGATTTTTTTTTATGAAGCGTTTATG
CTGACTCGTGCTCACTGAGCCAAGTGTGCATGGTCTGTTAGCTACTTTGTGGGTTCTTCTTT
CTTTCTACCCCTACTTCTTCCCTTTCCACCCCCCTAACACTAGATAGGAGAGAGGAGAGAGA
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTGAGT
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTCTTCTTGTCTTCTTCTCGCC
CACGACCACTTCACAAACACCGACCAACAGCAAACAACAACCCACCCCGCTTCTCGGGGG
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATCCAATCATCACACACTCAGAG
AAACTGTCTGCTGCTGGCAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCCACACCTGAGATTAAACAAAAACATT
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG
AGATTGTGGCTGTCTAGAGATTTTTGGAACAGCAAGTTGAAGGAACTTTCTTACCTGCCT
TGAATGGTGTCTTGAACCTTCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT
GTCCCCCTGTACCGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAAA
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG
GAACCAGGAGTTCAGGGTTATCCTGGGCTATATACCGTGACCCTGTCTACCCCCACACCC
CAATAAAAAAACAAAAAGGTC

SEQ ID NO: 104_SGK071_2_H

GAGGTGGTGGCTGTGCAGATGATGGTGGAAATGCATGGATGACCATTACGCCAGTCAGGCC
CTGGAGGAGCTGATGCCACTGCTGAAGCTGCGGCACGCCACATCTCTGTGTACCAGGAG
CTGTTTCATCACGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGATGGAGTTC
AATGAGCTCAGCTTCCAGGAGGTCATTGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC
TCTGAGTGGATGCAGAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT
TTGGACATCATCCACAGGAATCTCAAACCCCTCCAACATCATCCTCATCAGCAGTGACCAC
TGCAAACTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT
CGTGCGGAGGAAGACCCCTTTTCGTAAGTCTTGGATGGCCCCCTGAAGCCCTCAACTTCTCC
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC
TCCTTCATGGATGGCACAGAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCCAGGC
AGCCTGAAGGCCGTCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC
AGGAATCTTCTGCCCTTGATGCTCCAGATCGACCCCTCGGATCGAATAACGATAAAGGAC
GTGGTGACATCACCTTCTTGAGAGGCTCCTTCAAGTCTCTCGTGCCTCTCTGACCCTG
CACCGGCAGATGGTGCCTGCGTCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC
ATTTTAGGTGATGCTGGGGACACAAAGGGGGAGCGTGCCCTGAAGCTCCTGTCCATGGCC
TTGGCATCCTATTGTTTAGTTCCAGAGGGTTCATTATTTATGCCCCCTGGCCTTGCTCCAC
ATGCACGACCAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC
TCCCTGGGGAAACTAGGGAAGCTGTTGGGCCCCATCCCAAAGGGTCTGCCGTGGCCCCCG
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCCCTCGATGTCCAG
CTGTGTGCCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCACCCGGAA
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCCTGCTGAGTGCTCTTCAGAGCCAC
CCCGAGGAGGAGCCACTTCTTGTGATGGTCTACAGCCTGCTAGCCATCACCACAACCCAG

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FIGURE 2BBBB

GAGTCAGAGTCACTGTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA
AACCACGGAAAGCCCGGAAAACCCAAGAACCCTGCCAGCACCCAAAGTATCATTGTGAAC
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCCTGCG
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG
TCAGAGCTGGCGGCCTTCAAGGTGGTGGTGCAGGAGGAGGGCGGCAGTGGCCTCAGCCTC
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG
CTGCTGGTCCACCTGGCTTCCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTACCTCCAGCCTGGTGAGTGACAGCAGC
GCCTTCAGCAAACCAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT
GGGGGACTGGAATAG

SEQ ID NO: 105_AA118352_M SGK071_M

CAGAAGAAGACCCCTGCCAGAAGTCCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT
CCACCAAATCCGACATCTGGTCTCTGGGCTGCATCATTCTAGACATGGCCACTTGCTCCT
TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT
TAGGCAGCTGGCTGTGTGCTTCCTTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG
GCTCGCAGAGACTTGGGTTTGATTTTCAGTCAGTCTCTTGGACAGAGCACCCCTCTGAAAG
ATGTCATGCAGAATTTCTCCAGTCGACCAGAGGTCCAGCTCAGAGCCATTAACAAGTTGT
TGACAATGCCAGAGGACCAGCTAGGGCTGCCATGGCCACAGAGCTGCTGGAAGAGGTGA
TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC
TGCTGCGTGTTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA
GTTTGATCATCTCCTTCCTGATGGATACCTTGGCGAGCCATCCTAACTCTGAAAGGCTTG
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCTGGAGCACTTCCAAGAGGACA
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTCACTGGGTGCTGGCTACTCATC
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTGG
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA
AGGTGTCCGAAGTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCCTGAGGTGGTGGAGAACCCTCT
GCATGCTGTTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCTCTTCAGGC
CCTGACATGCTGCCCTTCTGGTCCCTGTGGTAAGAGAAAGTATCACTAGGTCCAGTATTAA
TTTCGTACCCCATGGTGACTAATAAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106_018653.9_H

GGCCGGGGTTCGGGGCGCGGGGCATGCGCGCGGGCTGGGCAGGGGGCCGGCCGGGGCGCAGA
GCGGAGCCGCCTCGGAGCCTGAGCCGCCCGGGGCGGGGAGCCCGCGGGGGCCG
GCCGGCCGGGGGAGGGGAGCGATGCGGCGCCGGCGGGCGGCAGTGGCCCGGGTTCCTG

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FIGURE 2CCCC

CGCCTCCTTCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTCCGAGCCTCCG
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTGCGGGGGCCGC
GGGGAGCTGGCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG
GGCCCCGGGCCCGGGGCGGGCCGGCCGGAGCGGCGGCCTGATGGACCTGGCTCCGGGC
GGGCCCGGCCTGCCGCGCCCCCGGCCCTTGGGCCCCGGCCCTGTCCGACGGCGCCCCA
GGCTGGCCCCCGGCTCCCGGCCAGGCTCCCCCGGCCGGGCCCGCGCCTGGGCTGCGCC
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC
CGGCTCCGCTGCCCGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC
GATCTGGGCAGCTGCGTGCGCGAGTTCCGGGTACGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGTCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAG
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCAGACACCCTGACCACCATCAG
GAGCTGGGCGCCCCGTAGAAAATGATCCAGCTGCTGCAAACTTCCTGGGAGGATCGATT
CGAATCTGCCTGAGCCTGGGCCGCTCCTCCACCACCTGGCCCACTCCCCACTGGGCTCC
GTCACCTCTGCTGGACTTCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA
CTCGAGTTTCCGGCCAGGAACCTTCAACCTGCCCTGCTCAGCCCAGGGCTGGTGCAGGGC
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTACATACCTCCTGCCT
CACAGTGCCCCGCTTCACTGCGTCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG
CTCGCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCGAGTGTATCCCA
GACAGCACCATCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC
CTCCTTTTCACTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCAGTGT
CGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCCGGCAGCTGGTCTTTTTCAAG
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCCTCTGGC
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCTGTG
GAGGGAGTGACTTGCACTGGCAGCACTGCATGTCACTGGGAACCCCTGCAGACAAAGCT
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAT
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT
GACTGCCTCTCCAACCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC
TGTGCCCTCCTCGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAATAGTGTGAGA
ATGTAGCTAAAGCCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGCTGCG
TGGGGACAATCCATCGTGGAGTGTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG
GGGACACTCCAGGCCAGCCCAGGGGTGAGGGGAGAGGTGCACACCTCAGCATGAGCCA
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG
GGCCTTTCTGCCTCATTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACAGGCTTTCC
CCCTTCCTCGAGTTTGAATATCCAGAATCTTTGTACTTCTTGTGTTAAATTGTTTAT
TTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACCTCTCCC
T

SEQ ID NO: 107_AA396601_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGCTGCGCGCGCAGTACGTGGGCTCAG
GCTACACTAAGGCTGTGTACCGGGTCCGCCTGCCCGGCGGCGCCGCGGTGGCGCTTAAAG
CAGTGGACTTCAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCGGGGCGCGAAGGG
GCTGCTATCGCCTGGCGGCCACAAGCTGCTCAAAGAGATGGTGTGCTGGAGCGGCTGC
GGCACCCTCAACGTGCTGAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCAG
ACACGCTGACCAACCATCAGAGCTGGGTGCCCTGTGGAGATGATCCAGCTGTTGCAGA
CTTCCTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCTCCTCCACCACCTGG
CCCACTCCCCGCTGGGCTCGGTACCCCTGCTTGAATTCGCGCTCGGCAGTTTGTGCTAG
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGGTGGAAGAGACACCGTGCA

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FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACCTTCAGCCTGCCCTGCTCGG
CCCAGGGCTGGTGCGAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT
TCTTCACATACCTCCTGCCACACAGTGCCCCGCCTTCCCTCCGACCTCTCCTGGATAGCA
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCAGCTGGAGA
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG
AGTACCAGCGCATCCCGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG
AGAGCCATGCTCAGTGTCTGTCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGA
AGCTGGTCTTTTTTAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT
ATGTGAAGGCCCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCCTGCTG
CAGGCGTGACTTGCATCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCAGAGCAA
CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAAATGTGAGTTTGCCAGC
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG
CTCAGGCTGGTCTTAAGTGGGACAGTCCCGTGGGCAGCCATTACTGCATTTCATGCTTTG
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTTCGGGGCCTCTCTG
CCTCATTTGCTTTTCAGTGAAAGCCAGGGAGCAGCCGAGCCAGGCTCCTCCCCTCCTGG
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC
CAGAAGCTTTTATACTTCTCGTTCATTAAATTGTTTATTTTGTAAAAAAAATTAAT
CAATTAATAAAATGATGTTTTGTGAC

SEQ ID NO: 108_VRK3_H

ATGATCTCCTTCTGTCCAGACTGTGGCAAAAGTATCCAAGCGGCATTCAAATTCCTGCCCC
TACTGTGGAAATTCTTTGCCGTGTAGAGGAGCATGTAGGGTCCCAGACCTTTGTCAATCCA
CATGTGTATCCTTCCAAGGCTCAAAGAGAGGGCTGAACTCCAGTTTGTAAACCTCTCCT
AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCCTCTGAGAGATCCAAAGGCTCCGGGAGC
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCACAGGGACAGTGCTGACAGAC
AAGAGTGGGCGACAGTGGAAGCTGAAGTCTTCCAGACCAGGGACAACCAGGGCATTCTC
TATGAAGCTGCACCCACCTCCACCCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG
GCCGCCAAGCCTCTGCAAGTCAACAAGTGAAGAAGCTGTACTCGACCCCACTGCTGGCC
ATCCCTACCTGCATGGGTTTCGGTGTTCACCAGGACAAATACAGGTTCTTGGTGTTACCC
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTGAGCCCAAAGCATGTGCTGTGAGAG
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCCTCCATGAGAAT
GAGTATGTTTCATGGAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAACACGTG
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTTCATTAGCATGGAC
CTGCACAAGGGATGCGGGCCCTCCCGCCGACGCACTCCAGAGCCTGGGCTACTGCATG
CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATGCCTTCCCAACACTGAGGACATC
ATGAAGCAAAAACAGAAAGTTTGTGATAAGCCGGGGCCCTTCGTGGGACCCCTGCGGTAC
TGGATCAGGCCCTCAGAGACCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCAGGTAT
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG
CGTGTGTCTCCATATGACCCATTGGCCTCCCGATGGTGCCCTAG

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FIGURE 2EEEE

SEQ ID NO: 109_S71575_M VRK3_M

CCATCCCCACCTGTATCGGCTTTGGCATTACCAGGACAAGTACAGGTTCCTAGTATTCC
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG
AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA
ATGAGTATGTTACGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA
GCCAGGTGACCCTGGTGGGCTATGGCTTACCTACCGATACTGCCAGGTGGCAAACACG
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG
ACCTGCACAAGGGATGCGGACCCTCCCGCCGAGCGATCTCCAGACCTTGGGCTACTGTA
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGATGGCCCTCAATT
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA
TGCGGGTGTACCCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG
CTTCCGACTTGACGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAAC
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTATGTAATGTGAAACTCCTCCCTGTCTC
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGCAGCAGCCAC
TCCACTCCCTATGGCATTCTGTGATGGCATAATAAACTGTTTTTAATC

SEQ ID NO: 110_AA45427_H

ATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAACCTGTCATCATTGACAATAAGCGCTAC
CTCTTCATCCAGAAACTGGGGGAGGGTGGGTTTCAGCTATGTGGACCTAGTGGAAGGGTTA
CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTACAGAGCAGCAGGACCGGGAG
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTCT
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG
ACCGAGGATCAAATCCTTTGGCTGCTGCTGGGGATCTGCAGAGGCCTTGAGGCCATTCAT
GCCAAGGGTTATGCCACAGAGACTTGAAGCCCACCAATATATTGCTTGAGATGAGGGG
CAGCCAGTTTTAATGGACTTGGGTTCATGAATCAAGCATGCATCCATGTGGAGGGCTCC
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCAGCGGTGCACCATCTCCTACCGAGCC
CCAGAGCTCTTCTCTGTGCAGAGTCACTGTGTATCGATGAGCGGACTGATGTCTGGTCC
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTCCAA
AAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGCATCCCAAAAGCCCCAGG
CATCTTCAGCATTGCGGCAGCTCCTGAAGTCAATGATGACCGTGGACCCGCATCAGCGT
CCTCACATTCTCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCAGCTCCTGGCCAA
CATACTACCCAAATCTGA

SEQ ID NO: 111_H05721_H

CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGACGCCGGTGGTGGCGGCAGC
GACGGCTGCGGGGGCACCGGGCCGCGGCCACCATGGCGGTGCGACAGGCGCTGGGCCG
CGCCTGCAGCTGGGTGAGCGCTGCTGCTGCGCTTACGGGCAAGCCCCGGCCGGGCCTA
CGGCTTGGGGCGGCGGGCCCGGCGGGCGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTCTGGGCTCGGGCTCCCTAACCGTCTCCGCTT
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGCTGTCAGCGGCAGTTCGTGGTGGCGGC
CTGGGCTGCGCGGGCCCTTGCGGCGGGCAGTCTTCTGGCCTTCCGGCTAGGGCTGGG
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGATCCA
GGCAATTTTTTACCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA
GGGCTTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGCTGC
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCCTGGAGGTGACAAAGAGCACCGG
GTTGCTTCCAGGGAGAGGCCAGGTACCAAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCC

FIGURE 2FFFF

GGGGGCCCCCTGCCTTCCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCCCTC
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTT
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC
CCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCGCTGCTGCC
AGGGGCCCCCTGGTCTGACTACCTTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG
CCATGGCCGGACGCTGTTCCCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG
CGTGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT
TGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCT
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGCGG
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCTGGCCCCAGGGCAGTGAT
TGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCT
TGTCATCCCTTCTACGGCCAGGGCAAGGCCCCACCTTGAAAGCCGAGCTACCAAGAGGC
TCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG
CTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTG
TGTGGAACAAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTGAAACGCTCTGCCA
GGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT
GAATTACTAAAAGAACATGGCATCCTCTGTGTCTGTGATGGTCTGTGAATGGTGAGGGTGG
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAAGAGCCCTCGGGCTTGG
CAAATGGAAGAACTTGAGTGAGAGTTTCACTCTGCAGTCCCTCTGCTCACAGACATCTGAAA
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTCACTGGCAGAGTTTGGCTGTGACCTTT
GCCCCCTAACACGAGGAACCTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG
GATGAAGGCAGACATCAACATGGGTGAGCACGTTTCACTTACGGGAGTGGGAAATTACATG
AGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTGGGGATTTAAACTTGAG
GGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAAATGCAAAATTACA
ACTGCAGATGACGTATGTGCCTTGAAGTGAATATTTGGCTTTAAGAATGATTCTTCTTAT
ACTCTGAAGGTGAGAAATATTTTGTGGGCAGGTATCAACATTGGGGAAAGAGATTTTATGTC
TAACTAACTAACTTTTATACATGATTTTTAGGAAGCTATTGCCTAAATCAGCGTCAACATG
CAGTAAAGGTTGTCTTCAACTGACAAAA

SEQ ID NO: 112_AI086865_H

AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG
CACCTGTGCCTGCGAAAGGCTGACCAGAAGCTGGTGATCATCAAGCAGATTCCAGTGGAA
CAGATGACCAAGGAAGAGCGGCAGGCAGCCAGAAATGAGTGCCAGGTCTCAAGCTGCTC
AACCACCCCAATGTCATTGAGTACTACGAGAACTTCTTGGAAAGACAAAGCCCTTATGATC
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTTATCCAAAAGCGCTGTAATTCC
CTGCTGGAGGAGGAGACCATCCTGCACTTCTTCTGTCAGATCCTGCTTGCATGCTCAT
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA
CACCGCATGGTCTCAAGATCGGTGATTTCCGCATCTCCAAGATCCTTAGCAGCAAGAGC
ACCCCATGCTATATCTCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAGAGTGAC
ATCTGGGCCCTGGGCTGTGTCCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTCGAGGCT
GCGAACTTGCCAGCACTGGTGTGTAAGATCATGAGTGGCACCTTTCACCTATCTCTGAC
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCTGAGTCTACTCAGCCTGGAGCCTGCCCAG
CGGCCACCACTCAGCCACATCATGGCACAGCCCCCTCTGCATCCGTGCCCTCCTCAACCTC
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACAGTGT
CCGCTGCAGAGAGGCATCATCATGACATTCCGCAGCGGCAGCAATGGGTGCCTAGGCCAT

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FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCACCATTTGTGGAGGCTTTGTTGGGCTATGAAATG
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACACTACTAGGCTCTGCACCCCTGGACCAG
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC
AAGTGTGCTGGAGACACAAGCAGTGCCTGGGCACATCATCTACCCTTTGCTCTGAC
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCACTGCAACTGTAATTCTAGGCTG
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGGGGCCAACCTGCTCCCATGTC
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT
GGCTGGTGCAAAGCTACAGACCTGTCTCTGTGGCAGTGATCCACCATCCACTCTACCAT
GAGTGTGGGGCAGATGATCTAAATGXXAAGAAGAGGAAGAGGAGGAGGAGGAAAAGCAAG
CCCCCATCCCGACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACCAGCATG
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAGGAAAAAGAGAAA
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAAGCCAAGAAAGGCCAGTTG
ACTAAGAAGAAAAGCCCGTTAAATTGGAGCCTTCCCGCCAGACGTGAGCCGATCATT
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCAGAAAGCCGGGAAGAGCTGGAG
AGCGAGGACAGTTACAATGGCCGGGGGAGGGAGAACTGTCCAGCGAGGATATTGTGGAA
TCATCATCGCCAGGAAGAGAGAGAAACACAGTCCAGGCCAAAAAGACAGGGGCAAAGCCC
TCACAAGCCAGGAAGGTAAACAAGAGAAAATCTCCCCAGGATCAAACCCCAACCTCAGT
TGAGGCCAGGGTGGTCAAGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG
CAGGGGTTTCTCAAAGGCAATCCAGCTTTCAAAAGGAAGCCCATGGGAAGGCAGGTGGG
AGGGAAGGAAGGGGCACAGCCCTATTTCTTCTACCTGCTAGGACAAGGTGGAAGAGTG
TATCTGGGGTGGGAAGGAGGGCTTCCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAT
CCACTTCTGGGACAGGCAGTACTGTCTGCAGCGATAACCCCAATAAACGGAACTTTTAA
CCC

SEQ ID NO: 113_AA836348_H

ATGTCGGTGCTGGGCGAGTACGAGCGACACTGCGATTCCATCAACTCGGACTTTGGGAGC
GAGTCCGGGGGTGCGGGGACTCGAGTCCGGGGCCTAGCGCCAGTCAGGGGCCGCGAGCC
GGCGGGCGCGCGGCGGAGCAGGAGGAAGTGCCTACATCCCCATCCGCGTCTGGGCGCG
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGACCGAGGATGACTCACTGGTTGTGTGG
AAGGAAGTCGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA
GTTATTCTGGCACTGCTGCAGCAGCACAACATTATTGCCTACTACAATCACTTCATGGAC
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC
CTTCGTCAGAAGGACAAGTTGTTTGAGGAAGAGATGGTGGTGTGGTACCTATTTTCAGATT
GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA
AATATTTTTCTGACCAAGGCAAACCTGATAAAACTTGGAGATTATGGCCTAGCAAAGAAA
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCCATATTACATGTCTCCA
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT
GTGAAGATCGTGCAAGGAATTCGGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA
TTGATCCAAATGGTTTCATTCGTGCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT
GAACCTCTAGATCGCCCTCTTCTCAGGAAACGAGGAGGTCAAGCACTGTGACTGAAGCA
CCCATTTGCTGTAGTAACATCACGAACAGTGAAGTCTATGTTTGGGGTGGTGGAATCC
ACCCCCAGAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG
AATACCCACTTTGCTGTGGTCACAGTGGAGAAGGAACTGTACACTTGGGTGAACATGCAA
GGAGGCACTAAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA
AAGCATGTGGAAAAGTTGCAAGGCAAAGCTATCCGTCAGGTGTGATGGTGATGATTTTC

FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACCTCTTC
CTCAGCAATCCAGTGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA
AACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTTCAGAA
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGAATTATCAACCATGAA
GCATACCATGAAGTTCCTTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT
AAGATCCGTACCATTTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG
CTGCTGACCTTTGGCTGCAACAAGTGTGGGCAGCTGGGCGTTGGGAACACAAGAAGCGT
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT
TCCAATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAAACTCCTGACCCA
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAAATCAGTCCC
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCTGGCTGGCTTCGAAAG
GAGCTGGAAAATGCAGAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG
TTTTCAGAATCTGAGAAAGATACCCTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAAGTGAAGCTTTTGGCC
TTTGAATCACAACCTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC
ACCACTGACTCCTCCTGCGTGTGCGTGACGCTCTCTGCAGGTGGAGGTTGA

SEQ ID NO: 114_R86668_H, MKK6_H

ATGAACCTTGCTGCTCTCCTACCGCGATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG
GAGACGCTGCAGGCCTTGCCACCTGTGATGTGGCCGAGCAGCATAATGTCTGCTTCCAC
TACACTTTTGGCCCTCAACCGGAGGAACAGGCCTGGGGACCGGGCGAAGGCCCTGTCTGTG
CTGCTGCCGCTGGTACAGCTTGAGGGCTCTGTGGCGCCCGATCTGTACTGCATGTGTGGC
CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCAGCCTTCACTCAGGCATCAAT
GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAAGAGCTCCGGCTA
ATAGGCATGAAGCTGGGCTGCCTGCTGGCCCCGAAAGGCTGCGTGGAGAAGATGCAGTAT
TACTGGGATGTGGGTTTCTACCTGGGAGCCAGATCCTCGCCAATGACCCACCCAGGTG
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCCATATGGTACCTGGTGTCCGTG
ATGGAGACCTTCCTGCTCTACCAGCACTTCAGGCCACGCCAGAGCCCCCTGGAGGGCCA
CCACGCCGTGCCCACTTCTGGCTCCACTTCTTGCTACAGTCTTGCCAACCATTCAGACA
GCCTGTGCCAGGGCGACAGTGCTTGGTGTGCTGGTCTGGAGATGAACAAGGTGCTGCTG
CCTGCAAAGCTCGAGGTTCTGGGGTACTGACCCAGTAAGCACAGTGACCCTGAGCCTGCTG
GAGCCTGAGACCCAGGACATTCCCTCCAGCTGGACCTTCCAGTCGCCTCCATATGCCGA
GTCAGCGCCTCAAAGCGCGACGAGCGCTGCTGCTTCTATGCACTCCCCCGGCTCAG
GACGTCCAGCTGTGCTTCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG
GCCTGGGTGACGAACCCGGATTCCACGGCGCCCGGAGGAGGCGGAGGGGGGAG
ATGTTGGAGTTTGATTATGAGTACACGGAGACGGGCGAGCGGCTGGTGTGGGCAAGGGC
ACGTATGGGGTGGTGTACGCGGGCCCGGATCGCCACACGAGGGTGCGCATCGCCATCAAG
GAGATCCCGGAGCGGGACAGCAGGTTCTCTCAGCCCCCTGCATGAAGAGATCGCTCTTCAC
AGACGCCTGCGCCACAAGAACATAGTGCCTATCTGGGCTCAGCTAGCCAGGGCGGCTAC
CTTAAGATCTTCATGGAGGAAGTGCCTGGAGGCAGCCTGTCTCCTGCTGCGGTGCGGTG
TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG
GGACTTGGCTACTTGACGACAACACATCGTGACAGGGACATAAAAGGGGACAATGTG
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG
GCAGGCATCACACCTTGCACTGAGACCTTCACAGGAACTCTGCAGTATATGGCCCCAGAA

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FIGURE 2III

ATCATTGACCAGGGCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC
ACTGTCAATTGAGATGGCCACAGGTGCGCCCCCTTCCACGAGCTCGGGAGCCACAGGCT
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCCAGCTCTCTGTGGCC
GAGGCCCCAAGCCTTTCTCCTCCGAACCTTTTGAGCCAGACCCCCGCTCCGAGCCAGCGCC
CAGACACTGCTGGGGGACCCCTTCTGTCAGCCTGGGAAAAGGAGCCGCAGCCCCAGCTCC
CCACGACATGCTCCACGGCCCTCAGATGCCCTTCTGCCAGTCCCACTCCTTCAGCCAAC
TCAACCACCCAGTCTCAGACATTCCCGTGGCCTCAGGCACCCTCTCAGCACCCACCCAGC
CCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTCCGGGGCTGAGCCTGCTGCACCAGGAG
AGCAAGCGTCCGGCCATGCTGGCCGCAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCGTCTGGGCAGAAACCATGTGGAA
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGGCAGCTCGCCAG
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGGCCAGGGCCTTGGGCCTGCGCTTCTGCAC
AGACCGCTGTTTGCCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT
CCACACTGGATGTTCTGTTCTGGACTCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT
GTGCTAGGACCGGAGGTGGAGAAGGAGGCGGTCTCACCAGGTCAGAGGAGCTGAGTAAT
GAAGGGGACTCCAGCAGAGCCAGGCCAGCAGAGCCCGCTTCCGGTGGAGCCCGAGCAG
GGCCCCGCTCCTCTGATGGTGCAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGCAGCGGGCTCTACAGCGG
CTGAATGAGGAAGCCCGGACCTATGTCTGGCCCCAGAGCCTCCAACCTGCTCTTTCAACG
GACCAGGGCCTGGTGCAGTGGCTACAGGAACTGAATGTGGATTGAGGCACCATCCAAATG
CTGTTGAACCATAGCTTACCCCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

SEQ ID NO: 115_PAK6_H

ATGTTTGGGAAGAAAAAGAAAAGATTGAAATATCTGGCCCCGTCCAACCTTTGAACACAGG
GTTTCACTACTGGGTTTGATCCACAAGAGCAGAAGTTTACCGGCCCTTCCCCAGCAGTGGCAC
AGCCTGTTAGCAGATACGGCCAACAGGCCAAAGCCTATGGTGGACCCTTCATGCATCACA
CCCATCCAGCTGGCTCCTATGAAGACAATCGTTAGAGGAAACAAACCCTGCAAGGAAACC
TCCATCAACGGCCTGCTAGAGGATTTTGACAACATCTCGGTGACTCGCTCCAACCTCCCTA
AGGAAAGAAAGCCCCACCCACCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG
GAAGAAAATGGCTTCATCACCTTCTCCAGTATTCCAGCGAATCCGATACTACTGCTGAC
TACACGACCGAAAAGTACAGGGAGAAGAGTCTCTATGGAGATGATCTGGATCCGTATTAT
AGAGGCAGCCACGCAGCCAAGCAAAATGGGCACGTAATGAAAATGAAGCACGGGGAGGCC
TACTATTCTGAGGTGAAGCCTTTGAAATCCGATTTTGCCAGATTTTCTGCCGATTATCAC
TCACATTTGGACTCACTGAGCAAACCAAGTGAATACAGTGACCTCAAGTGGGAGTATCAG
AGAGCCTCGAGTAGCTCCCTCTGGATTATTCAATTCCAATTCACACCTTCTAGAACTGCA
GGGACCAGCGGGTGCTCCAAGGAGAGCCTGGCGTACAGTGAAAGTGAATGGGGACCCAGC
CTGGATGACTATGACAGGAGGCCAAAGTCTTCGTACCTGAATCAGACAAGCCCTCAGCCC
ACCATGCGGCAGAGGTCCAGGTCAAGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA
GCAAGTGCAATTTAAACCCATCCCCAAGGACACTCCTACAACTCCTACACCTACCCTCGC
TTGTCCGAGCCCAATGTGCATTCCAAAGGTGGATTACGATCGAGCACAGATGGTCCCTC
AGCCCTCCACTGTGAGGTCTGACACCTACCCAGGGGCCCTGCCAAACTACCTCAAAGT
CAAAGCAAATCGGGCTATTCTCAAGCAGTCACCAGTACCCGTCTGGGTACCACAAAGCC
ACCTTGTACCATCACCCCTCCCTGCAGAGCAGTTTCGCAGTACATCTCCACGGCTTCCTAC
CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCAGCTGGGGCTCCTCCTCC
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGGCCCTGCAGCTGGTGGTC
AGCCCAGGAGACCCAGGGAATACTTGGCCAACCTTTATCAAAATCGGGGAAGGCTCAACC
GGCATCGTATGCATCGCCACCGAGAAACACACAGGGAAACAAGTTGCAGTGAAGAAAATG

FIGURE 2JJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT
TACCACCATGACAATGTGGTTGACATGTACAGCAGCTACCTTGTGCGCGATGAGCTCTGG
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAAGTTCTGAGAGCTCTCTCCTACCTTCAT
AACCAAGGAGTGATTACAGGGACATAAAAAGTGACTCCATCCTCCTGACAAGCGATGGC
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG
AAATCATTGGTTGGCACTCCCTACTGGATGGCCCTGAGGTGATTTCTAGGCTACCTTAT
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG
CCCCCTACTTCAATGAGCCTCCCTCCAGGCGATGCGGAGGATCCGGGACAGTTTACCT
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCTAGACTTGATG
TTGGTGAGGGAGCCCTCTCAGAGAGCAACAGCCAGGAACTCCTCGGACATCCATTCTTA
AAACTAGCAGGTCCACCGTCTTGCATCGTCCCCCTCATGAGACAATACAGGCATCACTGA

SEQ ID NO: 116_SURTK106_H

ATGAATGATAGGAATGAGATTCAAATGGAAGCCAACTCCAAAGTCTTACCATTATAGCA
CAGGAAATTTCTATGCAGATTCTTTATTACCCTTAGGAGACATGCACGTTTCTGCTCACT
AAACTAGGAAGGCAAGGAATGGCAAGGTGAGGAATTACTCACAGCTGTGCTGTGTGCATT
CTCTGTGGGCTTAGCAGGGAAGGGGACAGCCCTGTGGCAATGGGCATGACACGGATGCTC
CTGGAATGCAGTCTCAGTGACAAGTTGTGTGTGCATCCAGGAGAAGCAGTATGAAGTGATT
ATCGTCCCAACTTTGTTGGTTACTATCTTCTCATCCTTCTTGGGGTCATCCTGTGGCTT
TTTATCAGAGAACAAGAACTCAACAGCAGCGTTCTGGACCTCAAGGCATTGCCCCGTGT
CCTCCACCTAGGGACCTAAGCTGGGAAGCAGGACATGGAGGAAATGTGGCTTTGCCACTT
AAGGAGACATCCGTGGAACCTTTCTGGGAGCTACCACACCTGCCCTGGCTAAGCTGCAG
GTGCCGCGGGAGCAACTCTCTGAAGTTCTGGAGCAGATTTCAGTGAGTGTGGGCCCC
ATCTTTCGAGCCAATATGAACACTGGGGACCCCTTCTAAGCCCAAGAGTGTTATTCTCAAG
GCTTTAAAAGAACCAGCTGGGCTCCATGAGGTACAAGATTCTTAGGGCGAATCCAATTC
CATCAATACCTGGGGAAACACAAAAACCTGGTGCAGCTGGAAGGCTGCTGCACTGAAAAG
CTGCCACTCTATATGGTGTGGAGGATGTGGCCAGGGGGACCTGCTCGGCTTTCTCTGG
ACCTGTGCGCGGGATGTGATGACTATGGATGGTCTTCTCTATGATCTCACAGAAAAACAA
GTATATCACATCGGAAAGCAAGTCCTTTTGGCGCTGGAATTCCTGCAGGAGAAGCATTG
TTCCATGGGGATGTGGCAGCCAGGAATATTCTGATGCAAAGTGATCTCACTGCTAAGCTC
TGTGGATTAGGCCTGGCTTATGAAGTTTACACCCGAGGGGCCATCTCCTCTACTCAAACC
ATACCTCTCAAGTGGCTTGCCCCAGAACGGCTTCTCCTGAGACCTGCTAGCATCAGAGCA
GATGTCTGGTCTTTTGGGATCCTGCTCTATGAGATGGTGACTCTAGGAGCACCACCGTAT
CCTGAAGTCCCTCCTACCAGCATCCTAGAGCATCTCCAAAGAAGGAAAATCATGAAGAGA
CCCAGTAGCTGCACACATAACCATGTACAGTATCATGAAGTCCTGCTGGCGCTGGCGTGAG
GCTGACCGCCCCCTACCTAGAGAGCTGCGCTTGGCGCTAGAAGCTGCCATTAAAACCTGCA
GATGACGAGGCTGTGTTACAAGTACCAGAGTTGGTGGTACCTGAAGTGTATGCAGCTGTG
GCCGGCATCAGAGTGGAGAGCCTCTTCTACAACATATAGCATGCTTTGAAGAGTCTCGGGC
AAGAAACATTATGCATGAGTATATGTTCTTGGAAATCAATTCCTCTAAGAACAGAGAATG
GTCTTTCCAGGGACACAAAGGGAGAAATGGGACATGGATTCTTGATCTTCTTTACACA
TTTCTCGGGAAATCTGAAATGATGCTGGATGGGACTCTACACATCCTGAGCTAAGACATA
CTGTCAGTCTCACTTCTGCTGTCCCAGTCTTAGAAATCCTGGGTAGAAGTGGTGGACCTG
TGCAAAGGAGGTTTTAGAACTCTGCAGTATTTGTTGGGGCATGGCACAAATAAGCTCATC
CCTCCCGTCCGAGGCTAGTTTCTCTGGAACACATTTTATCTAGATGAAAATTTGGAA
TGAAATGAAGGAATAGAAATCCAATAAAAGAGTTGAAGGGAAAGAAAATTTAAGGTTCTT
CTTGCTCAGGATTACAGATATGGACCAACACCTCCTTCAAGAAAAGGTGGTAGGACACAA
AGTTCCTCAGTCCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC
TGAGTTTACCTTAGGTATAGATAAAAGAAAGATGGTCCCCCTTTATCTGATTCTGAGAC
AGGTAAATCTGTTTGTACTACGTTTAATTAGAAGGTGGAGGAGTCATTTATGATTAA

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FIGURE 2KKKK

GAACATTCAACATGTATTGTTTCATTAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAAAGAATTCTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGCACAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA
GTCTTTAACAAGGGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATT
TTCAATCATCTGTTGATATACTGTGAAACTTATTTTATTAAATTAATATTTATTAAATGG

SEQ ID NO: 117_AA098024_M

CTGCAGGAGAAGCACCTGTTTCATGGGGATGTGGCTGCCAGGAACATCCTGATCCAAAGT
GACCTGACTCCCAAACCTTTGTCATCTGGGCCTGGCTTATGAAGTTCATGCCCATGGGGCC
ATCTCCTCTGCTCGATCCAGCACCATCCCTCTCAAGTGGCTTGCTCCAGAAAGGCTTCTC
CTGAGACCTGCAAGCATCAGGGGAGATATTTGGTCCCTTTGGGATCCTGCTTTATGAGATG
GTGACTCTAGGAGCACCACCATAACCCTGAAGTCCCTCCCACCAGCATCCTACAATATCTT
CAGAGAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG
AAGTGCTGTTGGCGCTGGAGTGAGGACAGCCGCCCTTACTTGTTGAGCTGCTCCAGCGC
CTAGAAGCTGCTTCTAGATCTGCCGATGACAAGGCTGTGTTGCAAGTGCCAGAGTTGGTG
GTGCCTGAACTGTATGCAGATGTGGCTGGCATCAGGGCAGAAAGCATTTCCTATAGCTTC
AGTGTCTTTGAAGATGGTCCCTAGACAAATGACTATATATGGGTGGAATTAGTTCCTTCA
AGAACAGAGAGAAGGAACCTTTCTGTGGCCCAAGGGAGAAAAAGGACATGGATCTTG
CATCTTTCCCTAAACATTTTCTAGACATCTGAAATGCTGCTGGATGAAGCTCTACCTCT
ACATACCATGTACTCTTGAGCTAAGAATCACCATCAATTGTAGTTTGCTTTCCAGTCCCA
AGGGCTGAAGTATAAGTGGTGGACCGTGTCAATCTAAAGGAGGTTTTTAAATCTGCAAT
GATTGTAAGGGAATTAGGCAAAAGGGCTGGTCCCCTCACTCCAGGCTGGTTTACTACTG
AAACTAGTTTTTCTTTCTTTTTTTTTTAAAGTTAAACTATTACAGAGTAAAAATAAACAG
ATGGGCATGAATGAACACCTTCTAATTTTTTAACCATGAATTGAATATTGGAATTCATGAG
AAAGAAAATTCTAGGTTCTTTTTTGCTAAGAGGTGTTAAGGTGAGTCAATATATCCTTCAA
GGAAAGGCTTTGTCTCATCTATGTTGACGGGACGTAAAAGTCCCTCGTCCCGTTATGAAGA
GCTGAAGAAGATCTATAAGAAACAATACTGAGCCTTTCTTGACTATAGATAGAAGAGCA
TCCTTTTCATTGAACTCTGAGGCAGGTGGACCATGCATGATACTAAGTTAATTAGAAGCA
GGAGGAGTCATTTTCATGATTAGGAACATTGTTTCATCCCATTGTTTGCCAGTTCCTGTAA
GACTAAGGAGAATCAGCCTATAGAGCCAAAGCTAGAACCAGGGATAAAAAGTGTGTGTGT
GTATAACAAATAGGAAGCATGAAAGTCGAGCAAGAAGACTTAGTAACCCAGGTGGTCATT
AAGAGGTACAGAGAAGAAGTAATCTTATAGGAATGGATGGTAGCTTCTAATTTTTTAACCA
TTTCAGGTGTATAGCTGCCAAAATCTCTATAATAAAGAGGCTAAAAGAAAATAAATGGGA
GTTATTTTACTAGGAAAATTAGAGAACCTATAGTTTCCAAAAGAGATTCTTTATGTGCA
AAATGAGATAACTCTCTACCTCACAGGGTTGGTGTGAGGAACAATGAGAATATGTATTG
TGTATTATGTAGAATATAATATATTCTCAATAAATACTAGTTTTTCCCCTTTC

SEQ ID NO: 118_SGK2ALPHA_H

GAAGAGGGCAGAGCCGTGCATGGGGCTGCTCCCCAGGACCTGAGCAGGAACCTGGAGTTT
TCAGAGCTGCCTGATCATTGCTACAGAATGAACTCTAGCCAGCTGGGACCCCAAGTCCA
CAGCCCTCCAGGGCCAATGGGAACATCAACCTGGGGCCTTCAGCCAACCCAAATGCCAG
CCCACGGACTTCGACTTCCTCAAAGTCATCGGCAAAGGGAAGTACGGGAAGGTCTACTG
GCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGTGAAGGTACTACAGAAAAAGTCCATC
TTAAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAACGTG
CGGCACCCCTTCCTCGTGGGCCTGCGCTACTCTTCCAGACACCTGAGAAGCTCTACTTC
GTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCCGGTTC
CTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGTGGCCAGCGCCATTGGCTACCTGCAC
TCCCTCAACATCATTTACAGGGATCTGAAACCAGAGAACATTCTCTTGGACTGCCAGGGA
CACGTGGTGTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA

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FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT
GATCGAGCAGTGGACTGGTGGTGCTTGGGGGCGAGTCCCTCTACGAGATGCTCCATGGCCTG
CCGCCCTTCTACAGCCAAGATGTATCCAGATGTATGAGAACATTCTGCACCAGCCGCTA
CAGATCCCCGGAGGCCGGACAGTGGCCGCTGTGACCTCCTGCAAAGCCTTCTCCACAAG
GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCAACCAGGAAGCTGTG
TCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCA
TTCCTGGGATTTTCTTATGCGCCAGAGGATGATGACATCTTGATTGCTAGAGAAGAAG
ACCTGTGAAACTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGTAGGAA
GAGCGACTCAAATAACAATGGCTTCAACGAGAAGCAGGTTTATTTTTTCCAGCACATAA
AAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC
TGTATCTCTGCCCTGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTGCTACAAGATG
GTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAAATGGAGGAAAGGGGA
GAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAGCTCCCCCAATGACTTTTGCTT
CCATCTCACTAACCAACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCTTATTTGC
TGGGTACGTGACTATCCCTAATAACAAAGGGTTTTGACCCTAAGACATTAGGGGAGAAT
GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTGTTGGATTTTGATCT
CAATGTGTAAAATGACAGAGATGTAACAAGCTCATAGGGTATCAATATCTCTTATTGTTC
TATGTTGAAAAA

SEQ ID NO: 120_CCRK_H

ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGGCGCCACGGGCATCGTCTTCAAG
GCCAAGCACGTGGAGACTGGCGAGATAATTGCCCTCAAGAAGGTGGCCCTAAGGCGGTTG
GAAGACGGCTTCCCTAACCCAGGCCCTGCGGGAGATTAAGGCTCTGCAGGAGATGGAGGAC
AATCAGTATGTGGTACAACCTGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCC
TTTGAGTTTCATGCTGTGCGATCTGGCCGAGGTGGTGCGCCATGCCAGAGGCCACTAGCC
CAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCTCTTGCCATGCC
AACAACATTGTACATCGGGACCTGAAACCTGCCAACCTGCTCATCAGCGCTCAGGCCAG
CTCAAGATAGCGGACTTTGGCCTGGCTCGAGTCTTTTCCCCAGACGGCAGCCGCTCTAC
ACACACCAGGTGGCCACCAGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGGGTCC
CCCCTTTCCCCGGCAAGAACGATATTGAACAGCTTTGCTATGTGCTTCGCATCTTGGGC
ACCCCAAACCTCAAGTCTGGCCGGAGCTCACTGAGCTGCCGGACTACAACAAGATCTCC
TTTAAGGAGCAGGTGCCCATGCCCCCTGGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCA
TTGGATCTGCTGGGTCAATTCTTCTTACCCTCCTCACCAGCGCATCGCAGCTTCCAAG
GCTCTCCTCCATCAGTACTTCTTACAGCTCCCCCTGCCTGCCATCCATCTGAGCTGCCG
ATTCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGCCCCCCCCACATCCAT
GACTTCCACGTGGACCGGCTCTTGAGGGAGTCGCTGTTGAACCCAGAGCTGATTGGGC
CTTCATCCTGGAGGGGTGAGAAGTTGGCCCTGGTCCCGTCTGCCTGCTCCTCAGGACCAC
TCAGTCCACCTGTTCTCTGCCACCTGCCTGGCTTACCCTCCAAGGCCTCCCCATGGCC
ACAGTGGGCCCCACACCACACCTTGCCCCCTTAGCCCTTGCGAGGGTGGTCTCGAGGCAGA
GGTCATGTTCCAGCCAAGAGTATGAGAACATCCAGTCGAGCAGAGGAGATTATGGCCT
GTGCTCGGTGAGCCTTACCTTCTGTGTGCTACTGACGTACCCATCAGGACAGTGAGCTCT
GCTGCCAGTCAAGGCCTGCATATGCAGAATGACGATGCCTGCCTTGGTGTGCTTCCCCC
GAGTGTGCTCCTGGTCAAGGAGAAGTGCAGAGAGTAA

SEQ ID NO: 121_TESK2_H

GAATTCGCGCCGCTCGACGCTCAGCAGAGCTACCAGCTGCCCTGTTGGCTTCGCTGGTC
GGATCGTCTCCTGGCCCCGCCAAACAGCGGAGCGGGCCCCGACTGTGGGGCATGGCAGTA
GTCTCCTCGTCTCCGCCGCCGCTAGCCTAGCTGAGTCGCCGGCTTCTGCGCTAGGGGCT

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FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC
TCCCTCTTTGCCGCGTCTCCTCCTCTTGCCGCGCAGGCACCCCTCTGGCTGCTCAGTC
CTGCCTCAGTGTCAAACCAGAAGAGAAGTAAATTC AACAAAAATTTATGTGTGGAGTTC
CTTCTTAAAGAAGAAAAAGTGATTATTTAGACTATGGATCGGAGCAAACGGAATTC AA
TTGCAGGATTTCTCCACGTGTGGAGCGTCTTGAAGAGTTTGAAGGAGGTGGTGGAGGAG
AAGGAAATGTGAGCCAGGTGGGAAGAGTTTGGCCATCTTCGTATCGAGCTCTTATAAGTG
CCTTTTCCAGACTGACGCGTTTGGATGATTTACCTGTGAAAAATAGGGTCTGGCTTCT
TTTCTGAAGTGTTCAAGGTACGACACCGAGCTTCTGGTCAGGTGATGGCTCTTAAGATGA
ACACATTGAGCAGTAACCGGGCAAACATGCTGAAAGAAGTACAGCTCATGAATAGACTCT
CCCATCCCAACATCCTTAGGTATATCAACTCCGGGAACCTGGAACAGTTGCTAGACAGTA
ACCTGCCATTTGCCTTGGACTGTGAGGGTAAAACTGGCCTATGACATAGCAGTGGGCCTCA
GCTACCTTCACTTCAAAGGCATTTTTTCATCGGGACCTCACATCTAAGAACTGCCTGATAA
AGAGGGATGAGAATGGTTACTCTGCAGTGGTAGCTGACTTTGGCCTGGCTGAGAAGATCC
CCGATGTGAGCATGGGGAGTGAGAAGCTGGCCGTGGTGGGTTCCTTCTGGATGGCAC
CTGAGGTTCTCCGAGATGAGCCCTATAATGAAAAGGCAGATGTGTTCTCTTATGGTATCA
TCCTCTGCGAGATCATCGCCCGCATCCAGGCCGATCCGGACTATCTCCCCGCACAGAGA
ATTTTCGGGCTGGACTATGATGCTTTCCAGCACATGGTGGGAGACTGTCCCCCAGATTTTC
TGCAACTTACTTTCAACTGCTGTAACATGGATCCCAAACCTGCGCCCATCTTTTGTGGAGA
TTGGGAAGACCTTGAGGAAATTCTGAGCCGCTACAGGAAGAAGAGCAGGAGAGGGATA
GGAAGCTGCAGCCACAGCCAGGGGACTCTTGAGAAAGCACCTGGGGTGAAGCGACTAA
GCTCACTGGATGACAAGATCCCCACAAGTCACCATGCCCAAGACGTACCATCTGGCTGT
CTCGAAGCCAGTCAGATATCTTTTCCCGTAAGCCCCCACGTACAGTGAGTGTCTTGGACC
CATACTACCGGCCACGAGATGGTGTGCCCCGACCCCCAAAGTCAACCCTTTTAGTGCTC
GCCAGGACCTCATGGGGGGCAAGATCAAGTTTTTTGACCTGCCCAGCAAGTCTGTCTATCT
CTCTGGTATTTGACCTGGATGCACCAGGGCCCGAACTATGCCCCCTGGCTGACTGGCAGG
AGCCCCCTGGCCCCACCTATTGCGCGGTGGCGTTCCCTTGCTGGTTTCGCTGAGTTCTTGC
ATCAAGAGGCTTGTCCATTTGTGGGCCGGGAAGAATCGCTATCTGATGGGCCCCCACCAC
GCCTAAGTAGTCTCAAGTACAGAGTTAAAGAGATCCCACCATTCCGGGCATCTGCCCTAC
CAGCTGCTCAAGCCCATGAGGCTATGGACTGCTCCATTCTCCAGGAAGAAAATGGTTTTG
GGTCCAGGCCCCAGGGGACCAGTCCATGCCCTGCGGGTGCTTCTGAGGAGATGGAGGTAG
AAGAAAGGCCAGCAGGCTCAACTCCAGCCACCTTCTCCACCTCAGGCATAGGCCTGCAAA
CCCAGGGAAAGCAGGATGGGTGAGGGGGTTTAGTCCCTGCCTCACCTTGGGGATGGACCT
TCAGCTGAAACCATATGGCCCCCTAGGTGCACAGCCTTGATTCTTCCCTGGAGCCTACAG
AGCAGGCAGGCTAGGCCAAGCCAGGCTCAACTTCTGGGCTCCAGTGCCCATTTGGCTGTG
TATGACGGGAGGCAGCAGTGAGAGGCCTTCCTAGTTAGGGCCAAACAGCTGATACCAAGCC
TCTGAAATCCAGCAAGGAGGTCTGCCTCCACCAGACCCTCTCCAGTGTACTTCCCCAGA
TAGGACCAGAGGATGTCTAGTTCTAGGCTGAGCTGGCAGGCAGCTATTACCCCGGTTCTT
TCCCCACCCCAGGTCTGTCTCTTGCCTTTTCTTGGGGCATATAAGCTACTGAGTGGAACA
TGGAGCTGATCAAGAGGCCGTAATGGTTCATGGCTGTTTCCAGACCTGAATATTGGGTGCT
TCTTGCCAGTATTCTAAGACATTTGAGTAATTGCTGTTTGCACCTTACTGCATGGTCAGAC
CACGTCACTACATTTCTATGCAAGGGGACAGCAAGGCAGCGTGGTGGTTCATGGCTCTTAG
CTAACCTATTCAAAGACCTTTTCTGTTGATTAACTATTTTCATATTTATAAAGGAGTC
TTAATGTTCTGCCCCATAAGACTTTCAACCTTGTGGTTGGGAGTGGGGCTGGTTTTGTAG
GCCCTAGGGCCTGCTTCTATGTATTTATCAACATGTGATACATTCAATTGGTTAAATGGT
TTATACAGGGACTGATTTGCTTCCCTTCTGCCATGGCTGGAGCTTTGGGAACAGTCTGT
CCTTACAGAGCTGCAATAAGAAATAACCAAAGATGAAGCTGGTCAAATATTTTCATAACT
TGCTTCTGTTGATTTTTTTTTTGTAAAACTTTCCCAAGACATTTTCAGACTTAAAAATAA
AGTCAGTGTTACAGGT

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